

98	794.5	41.5	373	5	ABB91081	Abb91081	Herbicide
99	794.5	41.5	373	8	ADN74367	Adn74367	Thale cre
100	790.5	41.3	373	5	ABB91083	Abb91083	Herbicide

ALIGNMENTS

RESULT 1

AAV23342 standard; protein; 368 AA.

AAV23342;

01-SEP-1999 (first entry)

A bifunctional-O-methyl transferase involved in lignin production.

Bifunctional-O-methyl transferase; syringyl lignin; angiosperm; loblolly pine; Pinus taeda; lignin; woody plant; paper manufacture; delignification; pulp mill; gymnosperm.

Liquidambar styraciflua.

WO9931243-A1.

24-JUN-1999.

16-DEC-1998; 98WO-US026784.

16-DEC-1997; 97US-00991677.

(INTO) INT PAPER CO.

Chiang VL, Carraway DT, Smeltzer RH;

WPI; 1999-405034/34.

N-PSDB; AAX81875.

New DNA sequences encoding angiosperm enzymes involved in biosynthesis of syringyl lignin.

Example 1; Fig 2D-E; 83pp; English.

The present sequence represents a bifunctional-O-methyl transferase which is involved in syringyl lignin production in an angiosperm. The sequences are used to produce syringyl lignin in gymnosperms, especially the loblolly pine (Pinus taeda). It is necessary to remove much of the lignin from the fiber/lignin network of woody plants in paper manufacture. Greater proportions of syringyl lignin result in a higher delignification rate and hence a more efficient pulp mill operation

Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 2; Length 368;

Best Local Similarity 100.0%; Pred. No. 4.8e-196; Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSTSETKMSPEBA	AAAEAFV	FAMQ	LTSA	SVLP	PMV	LKSA	IELD	VL	ETMA	AG	PAHIS	60
DB	1	MGSTSETKMSPEBA	AAAEAFV	FAMQ	LTSA	SVLP	PMV	LKSA	IELD	VL	ETMA	AG	PAHIS	60
QY	61	TSDIASKLP	TKNPD	AAVMD	RLAS	SVLT	CS	RLTP	PD	KIR	LV	GLA	VCK	FTLN
DB	61	TSDIASKLP	TKNPD	AAVMD	RLAS	SVLT	CS	RLTP	PD	KIR	LV	GLA	VCK	FTLN
QY	121	DGVSIALSL	NODV	LVLM	ESWY	HL	TEA	VL	EG	IP	NK	AY	GT	AEYHGTDR
DB	121	DGVSIALSL	NODV	LVLM	ESWY	HL	TEA	VL	EG	IP	NK	AY	GT	AEYHGTDR
QY	181	GMSNSTIT	MKIL	ET	YK	FG	EG	IS	VVD	VG	GT	GA	HL	NI
DB	181	GMSNSTIT	MKIL	ET	YK	FG	EG	IS	VVD	VG	GT	GA	HL	NI

QY	241	APSYGV	HEVG	DM	VS	VP	K	GD	AI	FM	K	WT	CH	DM	S	DE	HL	CK	FL	K	C	Y	E	A	L	P
DB	241	APSYGV	HEVG	DM	VS	VP	K	GD	AI	FM	K	WT	CH	DM	S	DE	HL	CK	FL	K	C	Y	E	A	L	P

QY

301 ILPVA

301 ILPVA

361 IIEFLKXI 368

361 IIEFLKXI 368

AAAB19695 standard; protein; 368 AA.

AAAB19695;

05-FEB-2001 (first entry)

Sweetgum bifunctional O-methyltransferase.

Sweetgum; angiosperm; bifunctional O-methyltransferase; bi- gymnosperm; conifer; loblolly pine; transgenic plant; lignin

pulping.

Liquidambar styraciflua.

WO200058489-A2.

05-OCT-2000.

24-MAR-2000; 2000WO-US008083.

26-MAR-1999; 99US-00277248.

(INTO) INT PAPER CO.

Chiang VL, Carraway DT;

WPI; 2000-647240/62.

N-PSDB; AAA86683.

Use of angiosperm coniferyl aldehyde 5-hydroxylase which catalyzes the hydroxylation of coniferyl aldehyde, for modifying lignin b: gymnosperms, involves expressing the enzyme in a gymnosperm

Example 1; Page 61-64; 123pp; English.

The present sequence is that of sweetgum bifunctional O-methyl (b1-OMP), as deduced from an isolated cDNA clone (see AAA86683). The enzyme is involved in the syringyl lignin biosynthetic pathway. The invention is to identify, sequence and clone specific genes involved in the production of lignin, and to then introduce such genes into the genome of such as loblolly pine, to induce production of syringyl lignin thereby provide enhanced pulpability to the wood structure. Expression of the introduced angiosperm DNA, which is preferentially aldehyde 5-hydroxylase DNA (see AAA86682), is mediated by a gymnosperm promoter (see AAA86685-87) specific to genes involved in lignin biosynthesis

Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 3; Length 361

Best Local Similarity 100.0%; Pred. No. 4.8e-196; Matches 368; Conservative 0; Mismatches 0; Indels 3

QY	1	MGSTSETKMSPEBA	AAAEAFV	FAMQ	LTSA	SVLP	PMV	LKSA	IELD	VL	ETMA	AG	PAHIS	60
DB	1	MGSTSETKMSPEBA	AAAEAFV	FAMQ	LTSA	SVLP	PMV	LKSA	IELD	VL	ETMA	AG	PAHIS	60

QY 61 TSDIASKLPKPDAAVMDRLRLIASYSVLTCSLRTLPDCKIERLYGLAPVCKFLTEN 120
| | | | |
DB 61 TSDIASKLPKPDAAVMDRLRLIASYSVLTCSLRTLPDCKIERLYGLAPVCKFLTEN 120
| | | | |
QY 121 DGVSI AALSLMNQDKVLMESWYHLTEAVLEGIPPNKAYGWTAFEGHTDRFPTVFN 180
| | | | |
DB 121 DGVSI AALSLMNQDKVLMESWYHLTEAVLEGIPPNKAYGWTAFEGHTDRFPTVFN 180
| | | | |
QY 181 GMSNSTITMKKILETYGFEGLGSVDVGGTGAHLNMI IAKYPMIKGINFDLPVIE 240
| | | | |
DB 181 GMSNSTITMKKILETYGFEGLGSVDVGGTGAHLNMI IAKYPMIKGINFDLPVIE 240
| | | | |
QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCKCYEALPTNGKVI LAEC 300
| | | | |
DB 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCKCYEALPTNGKVI LAEC 300
| | | | |
QY 301 ILPVPDASLPTKAVVHIDVIMLAHNPCKERTKEFEALAKGAGFEGFRVVASCAVNTW 360
| | | | |
DB 301 ILPVPDASLPTKAVVHIDVIMLAHNPCKERTKEFEALAKGAGFEGFRVVASCAVNTW 360
| | | | |
QY 361 IIEFLKKI 368
| | | | |
DB 361 IIEFLKKI 368
| | | | |

RESULT 3
AAE05829
ID AAE05829 standard; protein; 368 AA.
AC AAE05829;

XX 24-SEP-2001 (first entry)
XX L. steyraciflua angiosperm bifunctional-O-methyl transferase (bi-OMT).
XX

KM Sweetgum; angiosperm, bifunctional-O-methyl transferase; bi-OMT;
KW syringyl lignin; gymnosperm; pulp; papermaking; guaiacyl lignin;
XX delignification.
XX

OS LiguIdambar steyraciflua.
XX

PN US6252135-B1.
XX

PD 26-JUN-2001.
XX

PF 16-DEC-1997; 97US-00991677.
XX

PR 16-DEC-1996; 96US-0033381P.
XX

PA (INTO) INT PAPER CO.
XX

PI Chiang VL, Carraway DT, Smeltzer RH;
XX

DR WPI; 2001-456503/49.
XX

DR N-PSDB; AAD11127.
XX

PT New P450-2 DNA encoding an enzyme involved in the biosynthesis of
PT syringyl lignin monomer units, for inducing the production of syringyl
PT lignin in gymnosperms and improving delignification for the production of
PT pulp.
XX

XX Example 1; Fig 2D-2E; 59pp; English.
XX

CC The invention relates to angiosperm sweetgum proteins bifunctional-O-
CC methyl transferase (bi-OMT); 4-coumarate CoA ligase (4CL); ferulic acid 5
CC -hydroxylase (P450-1 and P450-2) and their corresponding DNA molecules.
CC Angiosperm sweetgum proteins are useful for inducing the production of
CC syringyl lignin in gymnosperms for improved delignification in the
CC production of pulp for papermaking and other applications. The invention
CC also provides a method for modifying genes involved in lignin
CC biosynthesis in loblolly pine gymnosperms which involves cloning the
CC sweetgum DNA and fusing it to a constitutive promoter to form an

CC expression cassette. The expression cassette is then insert
CC gymnosperm genome, so that the production of syringyl lignin
CC while the production of guaiacyl lignin (less preferred for
CC suppressed. The present sequence is LiguIdambar steyraciflua
CC bifunctional-O-methyl transferase (bi-OMT) protein
XX

SQ Sequence 368 AA;
Query Match 100.0%; Score 1915; DB 4; Length 36
Best Local Similarity 100.0%; Pred. No. 4.8e-196;
Matches 368; Conservative 0; Mismatches 0; Indels s 0;

QY 1 MGSTSETKMSPEEAAAEAEAFVPMOLTSASVLRMYLKSATLELVLEIM IS 60
| | | | |
DB 1 MGSTSETKMSPEEAAAEAEAFVPMOLTSASVLRMYLKSATLELVLEIM IS 60
| | | | |
QY 61 TSDIASKLPKPDAAVMDRLRLIASYSVLTCSLRTLPDCKIERLYGL RN 120
| | | | |
DB 61 TSDIASKLPKPDAAVMDRLRLIASYSVLTCSLRTLPDCKIERLYGL RN 120
| | | | |
QY 121 DGVSI AALSLMNQDKVLMESWYHLTEAVLEGIPPNKAYGWTAFEGHGT NN 180
| | | | |
DB 121 DGVSI AALSLMNQDKVLMESWYHLTEAVLEGIPPNKAYGWTAFEGHGT NN 180
| | | | |
QY 181 GMSNSTITMKKILETYGFEGLGSVDVGGTGAHLNMI IAKYPMIKGI EE 240
| | | | |
DB 181 GMSNSTITMKKILETYGFEGLGSVDVGGTGAHLNMI IAKYPMIKGI EE 240
| | | | |
QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCKCYEALP EC 300
| | | | |
DB 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCKFLKCKCYEALP EC 300
| | | | |
QY 301 ILPVPDASLPTKAVVHIDVIMLAHNPCKERTKEFEALAKGAGFEGFR TW 360
| | | | |
DB 301 ILPVPDASLPTKAVVHIDVIMLAHNPCKERTKEFEALAKGAGFEGFR TW 360
| | | | |
QY 361 IIEFLKKI 368
| | | | |
DB 361 IIEFLKKI 368
| | | | |

RESULT 4
AD214866
ID AD214866 standard; protein; 368 AA.
XX
AC AD214866;
XX
XX 16-JUN-2005 (first entry)
XX
DE Syringyl lignin production-related protein, SEQ ID NO: 6.
XX
XX Syringyl lignin; genetic engineering.
XX
KW Paper; lignin; genetic engineering.
XX
OS Unidentified.
XX
XX US2005076403-A1.
XX
PN 07-APR-2005.
XX
PD 09-OCT-2003; 2003US-00681878.
XX
XX 16-DEC-1996; 96US-0033381P.
XX
PR 16-DEC-1997; 97US-00991677.
XX
PR 28-FEB-2001; 2001US-00796256.
XX
PA (CHIA/) CHIANG V L.
XX
PA (CARR/) CARRAWAY D T.
XX
PA (SMEL/) SMELTZER R H.
XX
PI Chiang VL, Carraway DT, Smeltzer RH;
XX
XX WPI; 2005-272442/28.
XX
DR N-PSDB; AD214865.

XX Modifying a gymnosperm genome, useful for enhanced pulpability for
PT papermaking, comprises inserting into the gymnosperm an expression
PT cassette having genes which code for enzymes that produce syringyl lignin
PT monomer units.

PS Claim 27; SEQ ID NO 6; 60pp; English.

CC The present invention relates to a method for modifying the genome of a
CC gymnosperm. The method involves inserting into the gymnosperm an
CC expression cassette, formed by fusing cloned angiosperm DNA sequences
CC which code for genes necessary for production of angiosperm syringyl
CC lignin monomer units to a promoter region associated with a gene. The
CC invention is useful for enhanced pulpability for papermaking. The present
CC sequence is the syringyl lignin production-related protein. Note: The
CC SeqID numbers given in the sequence listing do not correspond to the
CC SeqID numbers given in the claims and figure descriptions of the
CC specification.

XX Sequence 368 AA;

Query Match 100.0%; Score 1915; DB 9; Length 368;
Best Local Similarity 100.0%; Pred. No. 4.8e-196;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTETKMSPEEAAAEAEAFVPMQLTASVLPVLSAIELDVLTEIMAKAGGHAHS 60
DB 1 MGSTETKMSPEEAAAEAEAFVPMQLTASVLPVLSAIELDVLTEIMAKAGGHAHS 60
QY 61 TSDIASKLPPTKNPDAVWMDRLMLRLASYSVLTCSLRTPDGIKIRLYGLAFVCKFLTRN 120
DB 61 TSDIASKLPPTKNPDAVWMDRLMLRLASYSVLTCSLRTPDGIKIRLYGLAFVCKFLTRN 120
QY 121 DDGVSIALSLMNODKVLMSWYHLTEAVLEGGIPFNKAYGNTAFRYHGTDRFNTVFN 180
DB 121 DDGVSIALSLMNODKVLMSWYHLTEAVLEGGIPFNKAYGNTAFRYHGTDRFNTVFN 180
QY 181 GMSNSTITMKKILETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKINFDLPHVIEE 240
DB 181 GMSNSTITMKKILETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKINFDLPHVIEE 240
QY 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYBALPTNGXYILAEC 300
DB 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYBALPTNGXYILAEC 300
QY 301 ILPVPADASLPTKAVVHIDVIMLANHPPGKERTKEFEALAGAGFEGRRVVASCAVNTW 360
DB 301 ILPVPADASLPTKAVVHIDVIMLANHPPGKERTKEFEALAGAGFEGRRVVASCAVNTW 360
QY 361 IIEFLKKI 368
DB 361 IIEFLKKI 368

RESULT 5

ID AA01133 standard; protein; 365 AA.

XX AA01133;

DT 25-MAY-1999 (first entry)

DE Aspen bispecific O-methyltransferase (OMT).

XX OMT; woody plant; enzyme; O-methyltransferase; wood color; furniture;
KW paper industry; lignin; wood pulping; aspen bispecific OMT.

XX Populus tremuloides.

OS US5886243-A.

XX 23-MAR-1999.

XX

PF 18-SEP-1996; 96US-00715325.

XX 30-NOV-1995; 95US-0007727P.

XX (UNNT) UNIV MICHIGAN TECHNOLOGICAL.

XX Podila GK, Chiang VLC, Teal CJ;

XX WPI; 1999-228628/19.

DR N-PsDB; AAX26295.

PT Altering the wood color of a woody plant - by incorporating
PT methyltransferase gene into its genome, useful in the furni
PT industries.

PS Disclosure; Col 7-10; 9pp; English.

CC The invention relates to altering the wood color of a woody
CC incorporating a nucleotide sequence encoding the endogenous
CC enzyme O-methyltransferase (OMT) into its genome. Plants co
CC with altered wood color, are useful in the furniture and pa
CC and the modification of lignin caused by OMT (a reduction in
CC units) improves the efficiency of wood pulping. The present
CC represents an aspen bispecific OMT

XX Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 2; Length 36
Best Local Similarity 80.9%; Pred. No. 9.3e-162;
Matches 297; Conservative 37; Mismatches 30; Indels

QY 1 MGSTETKMSPEEAAAEAEAFVPMQLTASVLPVLSAIELDVLTEIM 60
DB 1 MGSTETKMSPEEAAAEAEAFVPMQLTASVLPVLSAIELDVLTEIM 60
QY 61 TSDIASKLPPTKNPDAVWMDRLMLRLASYSVLTCSLRTPDGIKIRLYGL 120
DB 61 TSDIASKLPPTKNPDAVWMDRLMLRLASYSVLTCSLRTPDGIKIRLYGL 120
QY 121 DDGVSIALSLMNODKVLMSWYHLTEAVLEGGIPFNKAYGNTAFRYHGT 180
DB 121 DDGVSIALSLMNODKVLMSWYHLTEAVLEGGIPFNKAYGNTAFRYHGT 180
QY 181 GMSNSTITMKKILETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKIN 240
DB 181 GMSNSTITMKKILETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKIN 240
QY 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYBAL 300
DB 241 APSYGVHEVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYBAL 300
QY 301 ILPVPADASLPTKAVVHIDVIMLANHPPGKERTKEFEALAGAGFEGRR 360
DB 301 ILPVPADASLPTKAVVHIDVIMLANHPPGKERTKEFEALAGAGFEGRR 360
QY 361 IIEFLKK 367
DB 361 IIEFLKK 364

RESULT 6

ID AA080015 standard; protein; 365 AA.

XX AA080015;

DT 15-JUL-2002 (first entry)

DE 5-hydroxyconiferaldehyde O-methyltransferase (AldOMT).

XX plant; aspen; phenylpropanoid pathway; agronomic; lignin; p
KW 4-conumate-CoA ligase; 4Cl; coniferyl aldehyde 5-hydroxylat
KW S-adenosyl-L-methionine-dependent; SAM; AldOMT; transgenic;

XX

KW 5-hydroxyconfederaldehyde O-methyltransferase; cellulose; pulp;
KM conferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD;
KM syringyl; guaiacyl; agriculture.
XX
OS Populus tremuloides.
XX
PN MO20020717-A2.
PD 14-MAR-2002.
PF 05-SEP-2001; 2001WO-US027445.
PR 05-SEP-2000; 2000US-0230086P.
PA (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
PI Chiang VLC, Li L;
XX MPI; 2002-351773/38.
XX N-PSDB; ABK48067.
PT Genetically transforming plant with multiple genes from phenylpropanoid
PT pathways, comprises incorporating number of genes into the genome of the
XX plant, to produce plants displaying altered agronomic traits.
XX
XX Example 2; Fig 4B; 95pp; English.
XX
XX The invention relates to a method of genetically transforming a plant
CC simultaneously with multiple genes from the phenylpropanoid pathways,
CC comprising incorporating into the genome of the plant, a number of genes,
CC their substantially similar fragments or their combinations, to produce
CC plants displaying altered agronomic traits. The genes are selected from 4
CC -coumarate-CoA ligase (4CL), conferyl aldehyde 5-hydroxylase (CA15H), S
CC -adenosyl-L-methionine (SAM)-dependent 5-hydroxyconfederaldehyde O-
CC methyltransferase (AldOMT), conferyl alcohol dehydrogenase (CAD) and
CC sinapyl alcohol dehydrogenase (SAD). The method is useful for the
CC transformation of plant tissue for the alteration of lignin monomer
CC composition, increased syringyl/guaiacyl (S/G) lignin ratio and increased
CC cellulose content and transgenic plants resulting from such
CC transformations. This is an improved method to simultaneously control the
CC lignin quantity, lignin compositions, and cellulose contents in plants,
CC and is applicable to all plant species that are susceptible to the
CC transfer of genetic information by Agrobacterium or other gene delivery
CC system. The method is of particular value to paper and pulp industries
CC because lignin containing higher syringyl monomer content is more
CC susceptible to chemical delignification. Woody plants transformed with
CC DNA constructs offer a significant advantage in the delignification
CC process over conventional paper feedstocks. Similarly, modification of
CC the lignin composition in grasses by insertion and expression of
CC heterologous SAD gene offers a unique method for increasing the
CC digestibility of grasses and is of significant potential economic benefit
CC to the farm and agricultural industries. The present sequence represents
CC the amino acid sequence of 5-hydroxyconfederaldehyde O-methyltransferase
CC (AldOMT) used in the method of the invention
XX
XX Sequence 365 AA:
SO
Query Match 83.3%; Score 1595.5; DB 5; Length 365;
Best Local Similarity 80.9%; Pred. No. 9.3e-162;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;
QY 1 MGSTSETMSESEAAAEERAPVPMQUTSASVPMVKSAIEIDVLEIMAKAGGAHIS 60
DB 1 MGSTGEOMTPTO--VSDDEBAHLFPMQJASASVLPMTIKTEIDLEIMAKAGGAPIS 58
QY 1 TSDTASTKLPFNKPAAVMLDRLMLTASVLTGSLRTLPQGIERYXGLAPVCKEFLRN 120
DB 59 TSEIASHLPFNKPAVMDRLMLTASVLTGSLRTLPQGIERYXGLAPVCKEFLRN 118
QY 121 DDGVSIALSIMNODKVLMSWYHLTEAVLEGGIPFNKAYGMTAFYHGTDPREVTVPNN 180
DB 119 EDGVSIVPLCLMNOQKVLMSWYHLKQALIDGGIPFNKAYGMTAFYHGTDPREVTVPNN 178

QY 181 GMSNHSITTMKKILFTTYGFEBSGVVDVGGTGALHNLNIAKYPMTIKCI
DB 179 GMSDHSITTMKKILFTTYGFEBSGLTLVDVGGTGAVVMTIVAKYPSIKCI
QY 241 APSYGEVHGDMVSVPKGDAIFMKWICHMSPDEHCKFLKCKYBALP
DB 239 APSYGEVHGDMVSVPKGDAIFMKWICHMSPDEHCKFLKCKYBALP
QY 301 ILVAPDASLPTRKAVHIDVIMLANPGKERTKEPEFALAKAGAFEGFR
DB 239 ILVAPDTSLATKGVVHVHIDVIMLANPGKERTKEPEFALAKAGAFEGFR
QY 361 IIEFLUK 367
DB 358 VIEFRKK 364
RESULT 7
ADD93900
ID ADD93900 standard; protein; 365 AA.
XX
XX ADD93900;
AC 29-JAN-2004 (first entry)
XX
XX 29-JAN-2004 (first entry)
DE Quaking aspen AldOMT protein.
XX
XX Quaking aspen; plant; enzyme; 4-coumarate-CoA ligase; 4CL;
KM conferyl aldehyde 5-hydroxylase; CA15H;
KM SAM-dependent 5-hydroxyconfederaldehyde O-methyltransferase;
KM S-adenosyl-L-methionine; AldOMT; conferyl alcohol dehydrog
KM sinapyl alcohol dehydrogenase; SAD; transgenic; agronomic p
KM lignin; cellulose; syringyl/guaiacyl lignin ratio; growth; w
KM stress resistance; sterility; grain yield; nutritional valu
KM paper delignification; pulp manufacture; grass digestibilit
XX
XX Populus tremuloides.
OS
XX US2002138870-A1.
PN
XX 26-SEP-2002.
PD
XX 06-MAR-2002; 2002US-00091009.
PF
XX 05-SEP-2000; 2000US-0230086P.
PR 05-SEP-2001; 2001US-00947027.
XX
XX (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
PA
XX Chiang VLC, Li L;
PI MPI; 2003-843045/78.
XX N-PSDB; ADD93899.
DR
XX Genetic transformation of plants, useful for altering ligni
PT cellulose contents, by introducing genes from the phenylpro
PT pathways, also new transgenic plants.
XX
XX Disclosure: SEQ ID NO 6; 55pp; English.
PS
XX The invention relates to the genetic transformation of a pl
CC simultaneously with several genes from the phenylpropanoid
CC incorporating into the genome the genes for 4-coumarate-CoA
CC conferyl aldehyde 5-hydroxylase (CA15H), S-adenosyl-L-Met
CC hydroxyconfederaldehyde O-methyltransferase (AldOMT), confi
CC dehydrogenase (CAD) and sinapyl alcohol dehydrogenase (SAD)
CC fragments or combination to produce plants with altered agr
CC Also included are preparing plant cells that contain, in th
CC several DNA constructs containing one or more of the specif
CC preparing transgenic plants with altered lignin or cellulose
CC of the regenerated plant), transgenic plants produced by me
CC their progeny, plants that include in the genome a construct

EE 240
ED 238
EC 300
EC 298
TW 360
TH 357
AD;
AD;
ity;
atio;

at least one of the specified gene (linked to a promoter and a terminator), a set of DNA constructs (each containing a promoter, and the set of above or a single construct containing the 4CL gene, where incorporated into a plant genome. The method is used to transform plants, particularly trees but also forage crops and monocotyledons, to alter their agronomic properties, especially lignin and cellulose contents, syringyl/guaiacyl (S/G) lignin ratio, growth, wood quality, stress resistance, sterility, grain yield and nutritional value, particularly to increase S/G ratio (this simplifies delignification in paper and pulp manufacture) and to increase digestibility of grasses. The present sequence represents quaking aspen Aldomt.

Sequence 365 AA;

Query Match 83.3%; Score 1595.5; DB 7; Length 365;
Best Local Similarity 80.9%; Pred. No. 9.3e-162;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

```

1 MGSTSETKSPSEAAAEBAFVPMOLTSASVLPVWVLSAIEDLVLEIMAKAGRGHIS 60
1 MGSTGETQMTPTQ--VSDEBAHLPFMOLASASVLPVWVLSAIEDLVLEIMAKAGRGHIS 58
61 TSDIASKLPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGKIBRLYGAPVCKFLTRN 120
59 TSEIASHLPTKNPDAPVWLDRLRLASYSILTCSLKDLPGDKVERLYGLAPVCKFLTRN 118
121 DDGVSIALLSMNODKVLMESEWYHLTEAVLEGGIFPNKAYCGMTAFENYGTDPREYTVNN 180
119 EDGVSVSPLCLMNODKVLMESEWYHLKDAILDGGIFPNKAYCGMTAFENYGTDPREYTVNN 178
181 GMSNSTITMKKILETYKGFEGLSVVDVGGGTGAHLNMIITAKYPMIGINDLPHVLEE 240
179 GMSDSTITMKKILETYKGFEGLSVVDVGGGTGAHVNTTVSKYISIGINDLPHVLEE 238
241 APSYGVHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKVIILAE 300
239 APSYGVHVGDMFVSVPKADAVFMKWI CHDMSDAHCKFLKNCYDALPEKGVILVEC 298
301 ILPVPADSLPTKAVVHIDVIMLANPGKERTKTEFEFALAKGAFEGFRVVASCAQNTW 360
299 ILPVPADTSLATKGVVHVDVIMLANPGKERTKTEFEFALAKGAFEGFRVWC-CAPNTW 357
361 IIEFLKK 367
358 VIEFLKK 364

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RESULT 8
AA030114
AA030114 standard; protein; 365 AA.

```

AC AA030114;
AC XX
DT 03-SEP-2003 (first entry)
DT XX
DE Strawberry O-methyltransferase (STOMT).
DE XX
KW Strawberry; O-methyltransferase; 2,5-dimethyl-4-hydroxy-3 (2H) -furanone;
KW STOMT; DMHF; dihydrochalcone; 2,5-dimethyl-4-methoxy-3 (2H) -furanone; DTF;
KW DMHF; enzyme; plant.
KW XX
OS Fragaria x ananassa.
OS XX
PN WO2003046163-A2.
PN XX
PD 05-JUN-2003.
PD XX
PF 26-NOV-2002; 2002MO-EP013320.
PF XX
PR 26-NOV-2001; 2001US-0332534P.
PR XX
PA (UYBA-) UNIV BAYERISCHE JULIUS MAXIMILIANS WUERZ.
PA XX

```

xx Schwab W, Kaldenhoff R, Wein M;
xx MPI; 2003-532772/50.
xx N-PSDB; AAL60735.
xx Novel isolated strawberry O-methyltransferase polypeptide u
xx methylating ortho-dihydroxy substituted ring system such as
xx caffeic acid, protocathechin aldehyde or pyrogallol.
xx Claim 1; Page 76-77; 78pp; English.

xx The invention relates to novel strawberry O-methyltransferase;
xx polypeptides capable of methylating an ortho-dihydroxy subst
xx system and nucleic acid molecules encoding such polypeptide
xx invention is useful for methylation of an ortho-dihydroxy su
xx ring system and/or its mimetics (such as 2,5-dimethyl-4-hy
xx furanone (DMHF) or dihydrochalcone (DHC)). The invention is
xx for the synthesis of naturally occurring substances preferal
xx compounds such as 2-methoxyphenol, vanillin, ferulic acid,
xx DMHF, for enhancing the function of naturally- occurring STY
xx or tissue cultured cells, or to enhance the production of f
xx enhancing substances such as vanillin or 2,5-dimethyl-4-met
xx furanone (DMHF). The present sequence is Fragaria x ananassa
xx O-methyltransferase

Sequence 365 AA;

Query Match 83.0%; Score 1589.5; DB 6; Length 36
Best Local Similarity 81.0%; Pred. No. 4.1e-161;
Matches 298; Conservative 39; Mismatches 28; Indels

```

1 MGSTSETKSPSEAAAEBAFVPMOLTSASVLPVWVLSAIEDLVLEIM 60
1 MGSTGETQMTPTQ--VSDEBAHLPFMOLASASVLPVWVLSAIEDLVLEIM 58
61 TSDIASKLPTKNPDAAVMDRLMLRLASYSVLTCSLRTPDGKIBRLYG 120
59 PSDIASQLPTKNPDAPVWLDRLMLRLASYSILTCSLRTPDGKVERLYCL 118
121 DDGVSIALLSMNODKVLMESEWYHLTEAVLEGGIFPNKAYCGMTAFENYGT 180
119 EDGVSIALCLMNODKVLMESEWYHLKDAILDGGIFPNKAYCGMTAFENYGT 178
181 GMSNSTITMKKILETYKGFEGLSVVDVGGGTGAHLNMIITAKYPMIGIN 240
179 GMSDSTITMKKILETYKGFEGLSVVDVGGGTGAHVNTTVSKYISIGIN 238
241 APSYGVHVGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP 300
239 APQYGVHVGDMFVSVPKGNALFMKWI CHDMSDEHCLKFLKNCYDALP 298
301 ILPVPADSLPTKAVVHIDVIMLANPGKERTKTEFEFALAKGAFEGFR 360
299 ILPVPADTSLATKGVVHVDVIMLANPGKERTKTEFEFALAKGAFEGFR 357
361 IIEFLKKI 368
358 VIEFLKKI 365

```

RESULT 9
AAW84132
AAW84132 standard; protein; 365 AA.

```

AC AAW84132;
AC XX
DT 11-FEB-1999 (first entry)
DT XX
DE Exemplary caffeic acid methyl transferase COMT sequence.
DE XX
KW (iso) eugenol methyl transferase; IEMT; lignin reduction;  
KW phenylpropanoid biosynthetic pathway; methyl-isoegenol;  
KW XX

```

KM caffeic acid methyl transferase; COMT.
XX
OS Unidentified.
XX
PN MO980570-A2.
XX
PD 12-NOV-1998.
XX
PF 08-MAY-1998; 98WO-US009522.
XX
PR 08-MAY-1997; 97US-0046857P.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Picheraky E, Wang J;
XX
XX WPI, 1998-610385/51.
XX
DR New isolated (iso)eugenol methyl transferase nucleic acids - used for
PT increasing methyl-isoegenol, decreasing the (iso)eugenol content of, or
PT decreasing lignin biosynthesis in, plants.
XX
XX Disclosure; Page 123-124; 151pp; English.
XX
XX The present sequence represents an exemplary caffeic acid methyl
CC transferase COMT sequence. The specification describes a Clarks breweri
CC (iso) eugenol methyl transferase (IEMT) enzyme. IEMT catalyses the
CC methylation of the para-4'-hydroxyl of both eugenol and isoeugenol to
CC methyl-eugenol and methyl-isoegenol, and participates in the
CC phenylpropanoid biosynthetic pathway. The IEMT nucleic acid can be used
CC for increasing the synthesis of methyl-isoegenol in plant cells or for
CC decreasing the (iso)eugenol content of plant cells. IEMT expression or
CC overexpression may facilitate the increased production of other desirable
CC products such as vanillin. The nucleic acids can also be used for
CC producing plants with a reduced amount of lignin which would be more
CC efficiently used as crop plants or fodder plants and which may have
CC increased yields when lignin has a negative effect on plant growth
XX
XX Sequence 365 AA;

Query Match 83.0%; Score 1588.5; DB 2; Length 365;
Best Local Similarity 80.7%; Pred. No. 5.2e-161;
Matches 296; Conservative 37; Mismatches 31; Indels 3; Gaps 2;
QY 1 MGSTSETMSPSEAAAEBAFVPMQUTSASVLPMLKSAIEDVLEIMAKAGAHIS 60
DB 1 MGSTGETMTPTQ--VSDDEAHLFAMQLASASVLPMLKTAIEIDLLEIMAKAGAHIS 58
QY 61 TSDIASKLPTKNPDAVWLDMLRLASYSVLTCSLRPLPGKIRLGLAPVCKFLTRN 120
DB 59 TSEIASHLPTKNPDAVWLDRLRLASYSILTCSLKPLPGKVRRLGLAPVCKFLTRN 118
QY 121 DDGVSIALLSINODKVLMSWYHLTEAVLBCGIPFNKAYGMTAFEGYGTDPREFTVFN 180
DB 119 EDGVSVSPLCLMNGDKVLMESWYILKDAILOGGIPFNKAYGMTAFEGYGTDPREFTVFN 178
QY 181 GMSNHSITTMKKIILETYKGFEGLSVVDVGGGTGAHLNMIATKPYMKIGINFDELPHVIEE 240
DB 179 GMSHSITTMKKIILETYKGFEGLSVVDVGGGTGAHVNTIVSKYPSIKGINFDELPHVIED 238
QY 241 APSYGVHVGDMFVSPKDAIFMKWICHDMSDEHLKFLKCYEALPTNKGKTIILAE 300
DB 239 APSYGVHVGDMFVSPKDAVFMKVICHDMSAHCLKFLKCYDALPENKGIILAE 298
QY 301 ILVPAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFRVVASCAVNTM 360
DB 299 ILVPAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFRVNC-CARFTH 357
QY 361 IIEFLKK 367
DB 358 VIEFRKK 364

RESULT 10
AAR34762
ID AAR34762 standard; protein; 364 AA.
XX
AC AAR34762;
XX
DT 25-MAR-2003 (revised)
DT 16-JUL-1993 (first entry)
XX
DE pPLC4 translation product.
XX
XX Plasmid, clone; pPLC4; transformation vector; CAD; enzyme;
KM caffeic acid O-methyl transferase; OMT; biosynthesis; diges
KM fodder; cattle; stalk strength; resistance; disease.
XX
OS Synthetic.
XX
PN MO9305160-A1.
XX
PD 18-MAR-1993.
XX
PF 09-SEP-1992; 92WO-GB001640.
XX
PR 10-SEP-1991; 91GB-00019279.
XX
PA (ICIL) IMPERIAL CHEM IND PLC.
XX
PI Van Doorselaere J, Fritig GJ, Inze DG, Jouanin L, Knig
PI Van Montagu M, Legrand M;
XX
DR WPI, 1993-100983/12.
DR N-PSDB; AA038448.
XX
PT DNA for modifying lignin content of plants - encodes o-meth
PT enzyme which can be enhanced or inhibited in plants, e.g. f
XX
PS Disclosure; Fig 1; 46pp; English.
XX
XX The sequence given represents the product of plasmid clone
CC can be used to produce a transformation vector for insertio
CC to regulate the production of the CAD enzyme. This sequence
CC caffeic acid O-methyl transferase (OMT) and can be used to
CC by modifying lignin biosynthesis. An anti-sense construct
CC sequence will down-regulate lignin synthesis. This is espec
CC for improving the digestibility of fodder crops for cattle.
CC production of lignin by a sense construct may improve plant
CC strength and resistance to disease. (Updated on 25-MAR-2003
CC field.)
XX
XX Sequence 364 AA;

Query Match 82.4%; Score 1578.5; DB 2; Length 3
Best Local Similarity 80.6%; Pred. No. 6.2e-160;
Matches 295; Conservative 36; Mismatches 32; Indels
QY 1 MGSTSETMSPSEAAAEBAFVPMQUTSASVLPMLKSAIEDVLEIM 1S 60
DB 1 MGSTGETMTPTQ--VSDDEAHLFAMQLASASVLPMLKTAIEIDLLEIM 1S 58
QY 61 TSDIASKLPTKNPDAVWLDMLRLASYSVLTCSLRPLPGKIRLGL 1N 120
DB 59 TSEIASHLPTKNPDAVWLDRLRLASYSILTCSLKPHPGKVRRLGL 1N 118
QY 121 DDGVSIALLSINODKVLMSWYHLTEAVLBCGIPFNKAYGMTAFEGYGT 1N 180
DB 119 EDGVSVSPLCLMNGDKVLMESWYILKDAILOGGIPFNKAYGMTAFEGYGT 1N 178
QY 181 GMSNHSITTMKKIILETYKGFEGLSVVDVGGGTGAHLNMIATKPYMKIGI 1E 240
DB 179 GMSHSITTMKKIILETYKGFEGLSVVDVGGGTGAHVNTIVSKYPSIKGI 1E 238
QY 241 APSYGVHVGDMFVSPKDAIFMKWICHDMSDEHLKFLKCYEALP 1E 300

Db	239	APSPBQVGHVGDGDMVSPKADAVVPMKRI	CHDMSAHCKLTKFKNCTYDALPENGKVIYEC	298
Qy	301	ILPVPADASLEPTKAVVHIDVIMALNPGGKERT	TEKEFEFALAKAGQFEGSPRVVASCAYNTW	360
Db	299	ILPVPADTSLATKGVVHIDVIMALNPGGKERT	TEKEFEFGLAKAGQFGSPBVMC-CAFNTW	357
Qy	361	IIIEFLK	366	
Db	358	VIEELRK	363	
RESULT 11				
ID	AAE16510			
XX	AAE16510	standard; protein; 365 AA.		
XX	AAE16510;			
AC	AAE16510;			
DT	09-APR-2002	(first entry)		
XX				
DE	Soybean caffeic acid 3-O-methyltransferase (COMT) #1.			
XX				
KW	Soybean; caffeic acid 3-O-methyltransferase; COMT; caffeic acid;			
KV	5-hydroxyferulic acid O-methyl transferase; phenylpropanoid;			
XX	transgenic plant; 5-hydroxyferulic acid; injury-repair mechanism;			
KX	papermaking; host defect repair mechanism; lignin biosynthesis.			
XX				
OS	Glycine max.			
XX				
PN	US6329204-B1.			
PD	11-DEC-2001.			
XX				
PP	09-FEB-2000; 2000US-00500569.			
XX				
PR	10-FEB-1999; 99US-0119587P.			
PA	(DUPO) DU POINT DE NEMOURS & CO E I.			
PI	Cahoon RE, Rafalski JA, Shen JB;			
DR	WPI; 2002-121138/16.			
DR	N-PSDB; AAD27040.			
XX				
PT	New polynucleotide encoding caffeic acid 3-O-methyltransferase from rice,			
PT	useful for studying lignin biosynthesis and in positive selection			
PT	systems.			
XX				
PS	Example 3; Page 27-30; 34pp; English.			
XX				
CC	The invention relates to an isolated nucleic acid fragment encoding			
CC	caffeic acid 3-O-methyltransferase (COMT) (also known as caffeic acid/5-			
CC	hydroxyferulic acid O-methyl transferase) involved in phenylpropanoid			
CC	metabolism. COMT is involved in the biosynthesis of the mono- or			
CC	dimethoxylated lignin precursors. COMT DNA is used to produce transgenic			
CC	plants or microbes that have altered levels of methylation for both			
CC	caffeic and 5-hydroxyferulic acids, so can provide a method for positive			
CC	selection. Since caffeic acid 3-O-methyltransferase is involved in lignin			
CC	biosynthesis, the transgenic plants may have altered contents, or types,			
CC	of lignin, so may be better suited for papermaking, and COMT DNA can also			
CC	be used to study synthesis of lignin in plant cells, including its role			
CC	in host defect- and injury-repair mechanisms. The present sequence is			
CC	soybean COMT protein			
XX				
XX				
SO	Sequence 365 AA;			
Query Match 81.8%; Score 1566.5; DB 5; Length 365;				
Best Local Similarity 80.2%; Pred. No. 1,2e-158;				
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;				
Qy	1	MGSISSETGMSSEAEAAAEFAVFPMQUTSASVLEWTLKSAIELDVLTIMAKAGCAHIS	60	
Db	1	MGSISGEITDITPTTH--VSDBEENLFFMQULASVLEWTLKSAIELDLTETINAKAGGVHLS	58	

Oy		61 ISDIASKPTKPPDAVWLDRLMLASLVYTCISLRTLPODKTERLYGL :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	N 120
Dd		59 PTDISQLPTONPPDAPVMLDRLLRLLACYNILSFSLRTPDPCKVRLEYGL :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	CN 118
Oy		121 DDGVALSILMNQOKVPMESGYHHLTEAVLEGCIFFPNKYAGMTAFEYHGTL :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	NN 180
Dd		119 EDGVSIALLNLNMNQKLMESEYYIKDALVEBGIEFPNNRYGGTAPEYHGTL :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	K 178
Oy		181 GMSNHSTITMKKILETYYKGFEGLSGVDVGCGTGALHNLIIAKYPMIKKII :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	E 240
Dd		179 GMADHSITITMKKIETTYGFESIAKSLVLVVGGCTGAIVINNIISKHPTKCII :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	SD 238
Oy		241 APSYGEVHEVGDDMVSPKGDATIMKWI CHDMWSBHCIFPKKCYEARLP :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	SC 300
Dd		239 APSYFGEVHEVGDDMASVPKDAILFMKWICHMWSBHCLKFKNCYTEALPI :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	SC 298
Oy		301 ILPVAPDASLPRTKAAVHHIDVIMLAHPGSKERTKEPFELAKAGAGEPR' :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	Fw 360
Dd		299 ILPVAPPSSIALTKGVHHIDVIMLANPRGKERTEKEPFELAKAGSGGR' :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	TN 357
Oy		361 IIIEFLKKI 368 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Dd		358 IMEFLEKI 365 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
RESULT 12			
AD129674			
ID	AD129674 standard; protein, 365 AA.		
XX			
AC	AD129674;		
XX			
DT	22-APR-2004 (first entry)		
DE	Soybean caffeic acid 3-O-methyltransferase homologue sequen		i .
XX			
KX	caffeic acid 3-O-methyltransferase; phenylpropanoid metabol		
KW	transgenic; plant; enzyme; soybean.		
XX			
OS	Glycine max.		
PX			
PN	US6610521-B1.		
PD			
XX	26-AUG-2003.		
Pf			
XX	05-OCT-2001; 2001US-00971823.		
XX			
PR	10-FEB-1999; 99US-0119587P.		
PR	09-FEB-2000; 2000US-00500569.		
PA	(DUPO) DU POINT DE MEMOURS & CO E I.		
XX			
PI	Cahoon RE;		
DR	WP1; 2003-895338/82.		
DR	N-PEDB; AD129673.		
PT			
PT	New polynucleotide having a sequence encoding a polypeptide		ltered
CC	caffeic acid 3-O-methyltransferase activity; useful for prok		
CC	levels of the protein involved in phenylpropanoid metabolist		
PS	transformed host cell.		
PS			
xx	Claim 4; SEQ ID NO 4; 35pp; English.		
CC	This invention relates to a novel isolated polynucleotide w		rises
CC	a nucleotide sequence or its complement encoding a polypept		ing the
CC	activity of caffeic acid 3-O-methyltransferase. The amino ac		nance
CC	of the polypeptide has at least 92% identity with the fully		365-
CC	amino acid sequence based on the clustal alignment method.		
CC	polynucleotide is useful for producing altered levels of th		
CC	involved in phenylpropanoid metabolism in a transformed hos		
SO	Sequence 365 AA;		

Query Match	81.8%; Score 1566.5; DB 7; Length 365;
Best Local Similarity	80.2%; Pred. No. 1.2e-158;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;	
QY	1 MGSTSETKMSPEAAAEBAFVPMQLTSAVLPMLKSAIELDVLEIMAKAGPGAHIS 60
DB	1 MGSTGETQITPTH--VSDBEANLPAMQLASASVLEMLKSALEDLLEIIAKAGPGAHIS 58
QY	61 TSDIASKLPKPNDAVAVMLDRMLRLIASYSVLTCSLRTLPGDKIERLYGLAVCYKFLTRN 120
DB	59 PTDISSQLPTQNPDAVPVMDRLRLRLACVNIISFSLRTLPGDKVERLYGLAVPAKYLVKN 118
QY	121 DDGVSIALSLMNOKVLMESWYHLTEAVLBEGIFPNKAYGNTAREYGTDRPTVFN 180
DB	119 EDGVSIALNLNODKVLMEWYTLKDAVLEGGIFPNKAYGNTAREYGTDRPTVFN 178
QY	181 GMSNSTITMKKILLETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKINPDLPHVIEE 240
DB	179 GMAHSTITMKKILLETYGFESLKSVDVGGTGAVINMIIVSKHTIKINPDLPHVIED 238
QY	241 APSYGEVHVGGDMFVSVPKGDALFMKWI CHDWSDEHCLKFLKCYEALPTNGKVI LAEC 300
DB	239 APSYGEVHVGGDMFVSVPKADALFMKWI CHDWSDEHCLKFLKCYEALPDNGKVI VAEC 298
QY	301 ILPVPDASLPKNAVYHIDVIMLANPBGKERTKEKFEFALAKGAGPEGRRVVASCAVNTW 360
DB	299 ILPVPDSSLATKGVVHIDVIMLANPBGKERTKEKFEFALAKGSGFQGRVVC-CAFTYN 357
QY	361 IIEFLKKI 368
DB	358 IMEFLKKI 365
RESULT 13	
ID	ADJ96484
ID	ADJ96484 standard; protein; 365 AA.
AC	ADJ96484;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Soybean caffeic acid 3-O-methyltransferase protein #1.
XX	
KW	Caffeic acid 3-O-methyltransferase; COMT;
KW	caffeic acid/5-hydroxyferulic acid O-methyltransferase;
KW	caffeoyl CoA 3-O-methyltransferase; COMT; lignin production;
KW	cell wall architecture; host defense; injury repair mechanism;
KW	transgenic plant; plant; soybean; enzyme.
XX	
OS	Glycine max.
XX	
PN	US2004014116-A1.
XX	
PD	22-JAN-2004.
XX	
PF	17-JUN-2003; 2003US-00464610.
XX	
PR	10-FEB-1999; 99US-0119587P.
PR	09-FEB-2000; 2000US-00500569.
PR	05-OCT-2001; 2001US-00971823.
XX	
PA	(CAHO/) CAHOON R E.
PA	(RAFA/) RAFALSKI J A.
XX	(SHEN/) SHEN J B.
XX	
P1	Cahoon RE, Rafalski JA, Shen JB;
XX	
XX	WPI; 2004-121565/12.
DR	N-PSDB; ADJ96483.
XX	
PT	New polynucleotide encoding a caffeic acid 3-O-methyltransferase
PT	polypeptide, useful in controlling lignin production in plant cells to
PT	control cell wall architecture and host defense and injury repair

PT	mechanisms in plant cells.
XX	
PS	Claim 10; SEQ ID NO 4; 38pp; English.
XX	
CC	The present invention relates to isolated polypeptide caffe
CC	methyltransferase (COMT) and the encoding polynucleotide. T
CC	otherwise termed as caffeic acid/5-hydroxyferulic acid O-
CC	methyltransferase and caffeoyl CoA 3-O-methyltransferase (C
CC	invention is useful in controlling lignin production in pla
CC	control cell wall architecture and host defense and injury
CC	mechanisms in plant cells. The invention is also useful in
CC	transgenic plants with altered level of methylation of caff
CC	hydroxyferulic acid. The present sequence is caffeic acid
CC	methyltransferase (COMT) protein.
XX	
SEQ	Sequence 365 AA;
Query Match	81.8%; Score 1566.5; DB 8; Length 3
Best Local Similarity	80.2%; Pred. No. 1.2e-158;
Matches 295; Conservative 41; Mismatches 29; Indels 3	
QY	1 MGSTSETKMSPEAAAEBAFVPMQLTSAVLPMLKSAIELDVLEIM 1S 60
DB	1 MGSTGETQITPTH--VSDBEANLPAMQLASASVLEMLKSALEDLLEI 1S 58
QY	61 TSDIASKLPKPNDAVAVMLDRMLRLIASYSVLTCSLRTLPGDKIERLYGL RN 120
DB	59 PTDISSQLPTQNPDAVPVMDRLRLRLACVNIISFSLRTLPGDKVERLYGL KN 118
QY	121 DDGVSIALSLMNOKVLMESWYHLTEAVLBEGIFPNKAYGNTAREYGT NN 180
DB	119 EDGVSIALNLNODKVLMEWYTLKDAVLEGGIFPNKAYGNTAREYGT NK 178
QY	181 GMSNSTITMKKILLETYKGFEGISVVDVGGTGAHLNMIIAKYPMIKI EE 240
DB	179 GMAHSTITMKKILLETYGFESLKSVDVGGTGAVINMIIVSKHTIKI ED 238
QY	241 APSYGEVHVGGDMFVSVPKGDALFMKWI CHDWSDEHCLKFLKCYEALP EC 300
DB	239 APSYGEVHVGGDMFVSVPKADALFMKWI CHDWSDEHCLKFLKCYEALP EC 298
QY	301 ILPVPDASLPKNAVYHIDVIMLANPBGKERTKEKFEFALAKGAGPEGRR TW 360
DB	299 ILPVPDSSLATKGVVHIDVIMLANPBGKERTKEKFEFALAKGSGFQGR TW 357
QY	361 IIEFLKKI 368
DB	358 IMEFLKKI 365
RESULT 14	
ID	AAR63203
ID	AAR63203 standard; protein; 365 AA.
AC	AAR63203;
XX	
DT	25-MAR-2003 (revised)
DT	10-MAY-1995 (first entry)
XX	
DE	Alfa1fa COMT.
XX	
KW	Alfa1fa; tobacco; Nicotiana tabacum; crop improvement; COMT
KW	caffeic-acid/3-O-methyltransferase; lignin; pCOMT; antisen
OS	Medicago sativa.
XX	
PN	WO9423044-A1.
XX	
PD	13-OCT-1994.
XX	
PF	31-MAR-1994; 94MO-US003356.
XX	
PR	02-APR-1993; 93US-00045263.

Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rag

ge 11

Search completed: December 12, 2005, 08:33:30
Job time : 194 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 08:27:04 ; Search time 39 Seconds
(without alignments)
907.892 Million cell updates/sec

Title: US-10-681-878a-6

Perfect score: 1915

Sequence: 1 MGSTSETKMSRSEAAAESE.....FRVASCANWTWIFLKKI 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR80:*

2: PIR1:*

3: PIR2:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1595.5	83.3	365	2	S18568
2	1544.5	80.7	365	2	T09673
3	1535	80.2	366	2	S40146
4	1527.5	79.8	359	2	T13259
5	1510	78.9	364	2	T09780
6	1499.5	78.3	364	2	S36403
7	1484.5	77.5	364	2	S16404
8	1403.5	73.3	350	2	T12260
9	1185	61.9	364	2	S28612
10	1062.5	55.5	365	2	J02344
11	1047	54.7	365	2	S22696
12	836	43.7	372	2	T09617
13	832	43.4	363	2	E96559
14	831.5	43.4	381	2	G96804
15	830.5	43.4	381	2	F96804
16	811.5	42.4	352	2	H86454
17	803.5	42.0	373	2	E86344
18	794.5	41.5	373	2	B86344
19	789.5	41.3	373	2	D86344
20	789.5	41.2	373	2	C86344
21	780.5	40.8	381	2	H96656
22	736.5	38.5	367	2	E96796
23	711	37.1	382	2	T09600
24	686.5	35.8	376	2	T06189
25	596	31.1	359	2	T46160
26	510	26.6	382	2	E96653
27	456	23.8	382	2	T04963
28	402	21.0	352	2	T09707
29	396.5	20.7	325	2	T04962

30	393	20.5	352	2	T09254	isoetl
31	378	19.7	364	2	U02268	O-met
32	376	19.6	360	2	T06786	6a-hy
33	369	19.3	390	2	S52015	chylt
34	354.5	18.5	343	2	T09299	catec
35	302	15.8	376	2	J01393	O-met
36	289	15.1	341	2	J05855	omyci
37	272.5	14.2	366	2	T01354	polyl
38	255.5	13.3	346	2	S21265	heidi
39	252.5	13.2	345	2	A42106	acety
40	252.5	13.2	494	2	S27696	acety
41	202.5	10.6	373	2	I37463	lcmt
42	186.5	9.7	356	2	A47128	acety
43	179.5	9.4	376	2	S49626	carri
44	179	9.3	334	2	F83120	crep
45	178	9.3	339	2	F70932	proba
46	174	9.1	393	2	S04408	hypot
47	171	8.9	379	2	T50751	hydro
48	159	8.3	292	2	J04099	hypot
49	158	8.3	390	2	T50880	hypot
50	139	7.3	339	2	C42276	hydro
51	116.5	6.1	270	2	E69303	O-met
52	111	5.8	1353	2	T00249	methy
53	105	5.5	352	2	E86015	methy
54	101.5	5.3	363	2	A10184	proba
55	100.5	5.2	308	2	S72886	proba
56	100.5	5.2	487	1	A64472	hypot
57	100	5.2	372	2	F64310	hypot
58	97.5	5.1	410	2	AB0077	proba
59	97	5.1	593	2	T04446	hypot
60	97	5.1	873	2	T12535	hypot
61	95.5	5.0	950	2	D81821	glyci
62	95.5	5.0	1447	2	T42628	lois
63	93.5	4.9	369	2	A75091	phosp
64	93.5	4.9	1916	2	S46157	RIF
65	93	4.9	379	2	A11526	hypot
66	92.5	4.8	379	2	A69516	proba
67	92	4.8	436	2	H70135	flage
68	91.5	4.8	329	1	A39440	aspar
69	91.5	4.8	353	2	E91169	proba
70	91.5	4.8	560	2	AB2437	NADH
71	91	4.8	197	2	AD2613	methy
72	91	4.8	197	2	B97395	phosp
73	91	4.8	679	2	S48939	hypot
74	90	4.7	745	2	B84673	hypot
75	89.5	4.7	357	2	E83205	hypot
76	89	4.6	244	2	F70072	conse
77	89	4.6	368	2	G86427	proba
78	89	4.6	384	2	S73122	catba
79	89	4.6	488	2	T09734	1-ami
80	89	4.6	1620	2	I51339	comp1
81	88.5	4.6	494	2	AD3255	1-8or
82	88	4.6	524	2	G86834	ydrog
83	87.5	4.6	556	1	A28185	alpha
84	87	4.5	1434	2	B36793	forma
85	86.5	4.5	351	2	B82496	hypot
86	86.5	4.5	405	2	H71620	immun
87	86.5	4.5	421	2	C71893	aspar
88	86.5	4.5	436	2	F69354	homos
89	86	4.5	295	2	AC3276	TRK P
90	86	4.5	319	2	AG1169	methy
91	86	4.5	446	2	AD0861	hypot
92	86	4.5	718	2	F90512	glyca
93	85.5	4.5	205	2	C75155	hypot
94	85.5	4.5	290	2	S45349	mechl
95	85.5	4.5	421	2	F64622	li me
96	85.5	4.5	448	2	G87482	homos
97	85.5	4.5	462	1	S29503	acety
98	85.5	4.5	462	1	B36786	mult
99	85	4.4	255	2	G97227	hypot
100	85	4.4	306	2	A72610	prote

ALIGNMENTS

RESULT 1

S18568
lignin-bispecific O-methyltransferase (EC 2.1.1.-) - quaking aspen
N:Contains: 5-hydroxyferulic acid O-methyltransferase (EC 2.1.1.-); caffeate O-methyltr
C:Species: Populus tremuloides (quaking aspen)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
R:Bugos, R.C.; Chiang, V.L.C.; Campbell, W.H.
Plant Mol. Biol. 17, 1203-1215, 1991
A>Title: cDNA cloning, sequence analysis and seasonal expression of lignin-bispecific ca
A:Reference number: S18568; MUID:92032785; PMID:1932694
A:Accession: S18568
A:Molecule type: mRNA
A:Residues: 1-365 <BUG>
A:Cross-references: UNIPROT:Q00763; UNIPARC:UPI0000127EA8; EMBL:X62096; NID:G20950; PIDN
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 63-Ser
A:Accession: S40017

A:Molecule type: protein
A:Residues: 165-184/335-346/349-359 <BD2>
A:Cross-references: UNIPARC:UPI00000A8C65; UNIPARC:UPI0000178C30; UNIPARC:UPI0000178C31
R:Bugos, R.C.; Chiang, V.L.; Campbell, W.H.
Phytochemistry 31, 1495-1498, 1992
A>Title: Characterization of bispecific caffeic acid/5-hydroxyferulic acid O-methyltrans
A:Reference number: A56669; MUID:92344802; PMID:1368360
A:Accession: A56669
A:Status: preliminary
A:Molecule type: protein
A:Residues: 165-184/335-346/349-359 <BUW>
A:Cross-references: UNIPARC:UPI00000A8C65; UNIPARC:UPI0000178C30; UNIPARC:UPI0000178C31
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: O-methyltransferase
C:Keywords: blocked amino end, lignin biosynthesis, methyltransferase; S-adenosylmethion

Query Match 83.3%; Score 1595.5; DB 2; Length 365;
Best Local Similarity 80.9%; Pred. No. 2.6e-123;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSSTETKSPSEAAAAEEAFVPMOLTSASVLPMTLSAIELDVLEIMAKAGRGATIS 60
DB 1 MGSSTETQMTPTQ--VSDEEAMLFAMQLASASVLPMTLTAIELDLEIMAKAGRGATIS 58
QY 61 TSDIASKLPTRKPDAAVMDRLRLASVYLTCSRLTPDGKIBRLVGLAVCKEFLTN 120
DB 59 TSEIASHLPTKPDAAVMDRLRLASVYLTCSRLTPDGKIBRLVGLAVCKEFLTN 118
QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGWTAFEPHGTDPREFTVFN 180
DB 119 EDGVSISPLCLMNODKVLMSWYLLDKDILDGIPFNKAYGWTAFEPHGTDPREFTVFN 178
QY 181 GMSNSTITMKKILETYKGFEGLSVVDVGGTGAAHLMITAKYPMIKGINFDLPHVIE 240
DB 179 GMSDSTITMKKILETYKGFEGLSVVDVGGTGAAVNTIVSKYPSIKGINFDLPHVID 238
QY 241 APSYGEVHVGDMPVSPKGDALFMKMICHDMSDEHCKLFLKCYEALPTNGKYLAE 300
DB 239 APSYGEVHVGDMPVSPKADAVFMKMICHDMSDEHCKLFLKNCYCDALPENKYLVE 298
QY 301 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGFEGFRVASCAYNT 360
DB 299 ILPVPADSLATKGVVHIDVIMLAHNPCKERTKEFEALAGAGFEGFRVASCAYNT 357
QY 361 IIEFLKK 367
DB 358 IIEFLKK 364

RESULT 2
T09673
caffeate O-methyltransferase (EC 2.1.1.68) - alfalfa
C:Species: Medicago sativa (alfalfa)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 1
C:Accession: T09673
R:Gowri, G.; Bugos, R.C.; Campbell, W.H.; Maxwell, C.A.; Dixon, J
Plant Physiol. 97, 7-14, 1991
A>Title: Molecular cloning and expression of alfalfa S-adenosyl-)
A:Reference number: 216815
A:Accession: T09673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-365 <GOW>
A:Cross-references: UNIPROT:P28002; UNIPARC:UPI00000433FC; EMBL:J
A:Experimental source: subspecies sativa, cultivar Apollo
C:Function:
A:Pathway: lignin biosynthesis
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 80.7%; Score 1544.5; DB 2; Length 3
Best Local Similarity 78.8%; Pred. No. 4e-119;
Matches 290; Conservative 42; Mismatches 33; Indels 2;

QY 1 MGSSTETKSPSEAAAAEEAFVPMOLTSASVLPMTLSAIELDVLEIM 15 60
DB 1 MGSSTETQITPTH--ISDEEAMLFAMQLASASVLPMTLSAIELDLEIT 15 58
QY 61 TSDIASKLPTRKPDAAVMDRLRLASVYLTCSRLTPDGKIBRLVGL 15 120
DB 59 PLEIASQLPTNPDAVMDRLRLALACVILITCSVVRQDGKVRVLGL 15 118
QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGWTAFEPHGT 15 180
DB 119 EDGVSIALSLNODKVLMSWYHLTKDAVLDGIPFNKAYGWTAFEPHGT 15 178
QY 181 GMSNSTITMKKILETYKGFEGLSVVDVGGTGAAHLMITAKYPMIGII 15 240
DB 179 GMSDSTITMKKILETYKGFEGLSVVDVGGTGAVNTIVSKYPTLIGII 15 238
QY 241 APSYGEVHVGDMPVSPKGDALFMKMICHDMSDEHCKLFLKCYEALP 15 300
DB 239 APSYGEVHVGDMPVSPKADAVFMKMICHDMSDEHCKLFLKCYEALP 15 298
QY 301 ILPVPADSLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGFEGFR 15 360
DB 299 ILPVPADSLATKGVVHIDVIMLAHNPCKERTKEFEALAGAGFEGFR 15 357
QY 361 IIEFLKKI 368
DB 358 IIEFLKKV 365

RESULT 3
S40146
catechol O-methyltransferase (EC 2.1.1.6) - cider tree
C:Species: Eucalyptus gunnii (cider tree)
C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 1
C:Accession: S40146
R:Grima-Petrenati, J.; Poeydomege, O.; Boudet, A.M.
submitted to the EMBL Data Library, August 1993
A:Reference number: S40146
A:Accession: S40146
A:Molecule type: mRNA
A:Residues: 1-366 <GR1>
A:Cross-references: UNIPROT:P46484; UNIPARC:UPI0000127EA5; EMBL:J
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 80.2%; Score 1535; DB 2; Length 366
Best Local Similarity 78.2%; Pred. No. 2.4e-118;
Matches 287; Conservative 45; Mismatches 31; Indels 3;

QY 1 MGSSTETKSPSEAAAAEEAFVPMOLTSASVLPMTLSAIELDVLEIT 15 59
DB 1 MGSSTETQMTPTQ--VSDEEAMLFAMQLASASVLPMTLSAIELDLEIT 15 58

C.Keywords: methyltransferase; S-adenosylmethionine

Query Match 78.3%; Score 1499.5; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 2e-115;
Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

QY 1 MGSTSETKMSPEBAALAEAEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHIS 60
DB 1 MGSTSETKMSPEBAALAEAEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHIS 58
QY 61 TSDIASKLPTKNDPAVMDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNN 120
DB 59 PSELAAQSLSTQNPBAFVMDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNN 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFN 180
DB 119 ADGVSAVAPLLANQDKVLMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFN 178
QY 181 GMSNSTIMMKKILLEYKGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIE 240
DB 179 GMSDSTMSMKKILLEYKGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIE 238
QY 241 ABSYGVHEVGGDMFVSVPGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAE 300
DB 239 APTYGVHEVGGDMFVSVPGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAE 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLANHPGKERTKEKFEALAGAGPFGF-RVVASCAVNT 359
DB 299 ILPEAPDTSLATKNTVHVIDVIMLANHPGKERTKEKFEALAGAGPFGFRLVALTLTGS 358
QY 360 W 360
DB 359 W 359

RESULT 7
S36404
catechol O-methyltransferase (EC 2.1.1.6) - common tobacco
C/Species: Nicotiana tabacum (Common tobacco)
C/Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S36404
R/legrand, M.
submitted to the EMBL Data Library, August 1993
A/Reference number: S36403
A/Accession: S36404
A/Molecule type: mRNA
A/Residues: 1-364 <LEG>
A/Cross-references: UNIPROT:Q04065; UNIPARC:UP100000A0CF72; EMBL:X74453; NID:G396590; PII
C/Superfamily: O-methyltransferase
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 77.5%; Score 1484.5; DB 2; Length 364;
Best Local Similarity 77.0%; Pred. No. 3.4e-114;
Matches 278; Conservative 38; Mismatches 42; Indels 3; Gaps 2;

QY 1 MGSTSETKMSPEBAALAEAEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHIS 60
DB 1 MGSTSETKMSPEBAALAEAEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHIS 58
QY 61 TSDIASKLPTKNDPAVMDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNN 120
DB 59 PSELAAQSLSTQNPBAFVMDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNN 118
QY 121 DDGVSIALSLNQDKVLMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFN 180
DB 119 ADGVSAVAPLLANQDKVLMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFN 178
QY 181 GMSNSTIMMKKILLEYKGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIE 240
DB 179 GMSDSTMSMKKILLEYKGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIE 238
QY 241 ABSYGVHEVGGDMFVSVPGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAE 300
DB 239 APTYGVHEVGGDMFVSVPGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAE 298

DB 239 APAYGVHEVGGDMFVSVPGDAIFMKWICHDMSEHCLKFLKNCYEALPJ 304 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLANHPGKERTKEKFEALAGAGPFGF-1 359 359
DB 299 ILPEAPDTSLATKNTVHVIDVIMLANHPGKERTKEKFEALAGAGPFGF-1 358 358
QY 360 W 360
DB 359 W 359

RESULT 8
T12260
caffeoyl-CoA O-methyltransferase (EC 2.1.1.104) - common ice plant
C/Species: Mesembryanthemum crystallinum (Common ice plant)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 1
C/Accession: T12260
R/Michalowski, C.B.; Bohnert, H.J.
submitted to the EMBL Data Library, March 1998
A/Description: Mesembryanthemum crystallinum caffeic acid 3-O-methyltransferase.
A/Reference number: Z17477
A/Accession: T12260
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-350 <MIC>
A/Cross-references: UNIPROT:O65362; UNIPARC:UP100000A4A72; EMBL:J
C/Function: 11gnln biosynthesis
A/Pathway: 11gnln biosynthesis
C/Superfamily: O-methyltransferase
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 73.3%; Score 1403.5; DB 2; Length 364;
Best Local Similarity 74.6%; Pred. No. 1.5e-107;
Matches 261; Conservative 46; Mismatches 42; Indels 1;

QY 18 BEEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHISDSDIASK 359 77
DB 1 BEEAFVPMQLTSASVLPWVLSAIELDVLEIMARAGPGAHISDSDIASK 358 77
QY 78 MLDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNDGVSILN 359 137
DB 61 MLDRLMLRLASVLTCSLRTLPDGIKIBRLYGLAVPCKFLTNDGVSILN 358 137
QY 138 LMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFNNGMSNST 359 197
DB 121 LMESWYHLTEAVLEGGIPFNKAYGMTAFREYHGTDRPNTVFNNGMSNST 358 197
QY 198 KGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIEBAPSYPGV 359 257
DB 181 KGFEGISVVDYGGGGAHLNMIITAKYPMIKGINFDLPVHIEBAPSYPGV 358 257
QY 258 VPKGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAECLIPVAPD 359 317
DB 241 VPKGDAIFMKWICHDMSEHCLKFLKCYEALPTNGKVIILAECLIPVAPD 358 317
QY 318 IDVIMLANHPGKERTKEKFEALAGAGPFGF-RVVASCAVNTIIEPLKX 359 300
DB 301 IDVIMLANHPGKERTKEKFEALAGAGPFGF-RVVASCAVNTIIEPLKX 358 300

RESULT 9
S28612
catechol O-methyltransferase (EC 2.1.1.6) - maize
C/Species: Zea mays (maize)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 1
C/Accession: S28612
R/Collazo, P.; Montoliu, L.; Puigdomenech, P.; Rigau, J.
Plant Mol. Biol. 20, 857-867, 1992
A/Title: Structure and expression of the 11gnln O-methyltransferase
A/Reference number: S28612; M01D:9309238; PMID:1463825
A/Accession: S28612
A/Molecule type: DNA
A/Residues: 1-364 <COL>

A:Cross-references: UNIPROT:Q06509; UNIPARC:UPI0000127EA6; EMBL:W73235; NID:g1256711; P	
C:Genetics:	
A:Introns: 141/2	
C:Superfamily: O-methyltransferase	
C:Keywords: methyltransferase; S-adenosylmethionine	
Query Match	
Best Local Similarity 61.9%; Score 1185; DB 2; Length 364;	
Matches 230; Conservative 51; Mismatches 77; Indels 14; Gaps 7;	
Qy	1 MGSTETKMSPEEAAAEAEAFVPMQLTSASVLPVYLKSAIELDVLEIMAK-AGPG-AH 58
Db	1 MGST-----AGVAAVVBEEACVMYMQLAASSILPMTLKNAELGLBVLQGEAGGKXA 55
Qy	59 ISTDIAASKLPKAPD---AAVMDRLMLASYSVLTCSLRTLDPDKIERLYGLAPVCK 115
Db	56 LAPBEVVAAMPAPBDPAALAAAVDRMLRLLASVDVVRQMED-RDGRERYSAAPCK 114
Qy	116 FLTRDDGVSIATSLMNDKYLMSWYHLTEAVLEGIPFKKAYGMTAFEHGTDPRFN 175
Db	115 WLTPEEDGVSMALALMNDKVLMSWYLLKDAVLGGIPFKKAYGMTAFEHGTDARFN 174
Qy	176 TVFNNGMSNSTITMKILLETYKGFEGLSVVDVGSGTAHLMITIAKYPMIKGINFDLP 235
Db	175 RVFNNGMKNHSYIIRKILDFYTGFEVSTLVVVGSGVATLHATSRPHISGVNFDLP 234
Qy	236 HVIEBAPSYPGVEHVGDMFVSVPKGDALFMKWLCHDMSDEHCLKFLKKCYEALPTNGKV 295
Db	235 HVISAPPEPFGVRAHVGDMFASVPAGDAILMKWILHDMSDALCATLLKCYDALPENGKV 294
Qy	296 ILAECILVAPDASLPTKAVVYHIDVIMLANHPGKERTKEFEALAKGAFSGPRVASC 355
Db	295 IIVBEVLVNTVTEATPKAGVFHVDIMLANHPGKERYERERELAKGAFSGPR--ATY 352
Qy	356 AY-NTWIEFLK 366
Db	353 IYANMAIEFIK 364
RESULT 10	
QJ02344	
cathchol O-methyltransferase (EC 2.1.1.6) III - common tobacco	
C:Species: Nicotiana tabacum (common tobacco)	
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004	
C:Accession: U02344; F00814	
R:Bellegri, L.; Geofroy, P.; Fritlig, B.; Legend, M.	
Plant Physiol. 103, 509-517, 1993	
A:Title: Molecular cloning and expression of a new class of ortho-diphenol-O-methyltrans	
A:Reference number: U02344; MUID:94302149; PMID:7518088	
A:Accession: U02344	
A:Molecule type: mRNA	
A:Residues: 1-365 <PEL1>	
A:Cross-references: UNIPROT:Q42949; UNIPARC:UPI00000ACCD; EMBL:X71430; NID:g429113; PID	
A:Accession: P00814	
A:Molecule type: protein	
A:Residues: 8-33,55-61,106-114,136-145,161-169,175-180,181-191,193-198,199-204,205-218,2	
A:Cross-references: UNIPARC:UPI0000178C32; UNIPARC:UPI0000178C33; UNIPARC:UPI0000178C34;	
C39; UNIPARC:UPI0000178C3A; UNIPARC:UPI0000178C3B; UNIPARC:UPI0000178C3C; UNIPARC:UPI000	
A:Experimental source: leaf, cv. Samsun NN	
C:Genetics:	
A:Gene: OMT	
C:Superfamily: O-methyltransferase	
C:Keywords: methyltransferase; S-adenosylmethionine	
Query Match	
Best Local Similarity 57.6%; Pred. No. 1.6e-79;	
Matches 212; Conservative 51; Mismatches 94; Indels 11; Gaps 7;	
Qy	5 SETKMSPEEAAAEAEAFVPMQLTSASVLPVYLKSAIELDVLEIMAKAGCAHISTSDI 64
Db	3 SSTK-SQIPTSEEBERNCTYAMQLSSSVLPVLTSTIQLEVEFIILAKSN-DTKLASQI 60
Qy	65 ASKLPK-KNPDAVVLDMRLRLASVLTCSLRTLPPD---GKIERLYGLAPVCKFLTR 119

Db	61 VSQINPCNPDATMLDRLRLVLAISVLTCSL--VEBENNCGGKRYTG	VR 118
Qy	120 NDDGVSIATSLMNDKYLMSWYHLTEAVLEGIPFKKAYGMT-AFEXH	VF 178
Db	119 DEDGASMGPLALLADKVPINSWFELKDAVLEGVPPFRVHGVNAFEP	VF 178
Qy	179 NNGMSNSTITMKILLETYKGFEGLSVVDVGSGTAHLMITIAKYPMIK	VI 238
Db	179 NQAMNHTTVWKKILEYKGFENLKTIVDVGGLGVMLKITSKPTIK	VI 238
Qy	229 BEAPSYPGVEHVGDMFVSVPKGDALFMKWLCHDMSDEHCLKFLKKCYEA	LA 298
Db	229 QHAPSYPGVEHVGDMFESVPEGDALFMKWLHDMSDSHNLKLLKCYKA	VV 298
Qy	299 ECILVPAPDASLPTKAVVYHIDVIMLANHPGKERTKEFEALAKGAFEG	YN 358
Db	299 EALLPVKPDIDPAVVGQCDLIMWAQNPGRKERESEERBALATAGFRG	CN 357
Qy	359 TWIIEFLK 366	
Db	358 FWMMEFCK 365	
RESULT 11		
S22696		
myo-inositol O-methyltransferase (EC 2.1.1.-) IMT1 - common ice		
C:Species: Mesembryanthemum crystallinum (common ice plant)		
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change		
C:Accession: S22696; S66386		
R:Vermon, D.M.; Bohnert, H.J.		
EMBO J. 11, 2077-2085, 1992		
A:Title: A novel methyl transferase induced by osmotic stress in		
A:Reference number: S22696; MUID:92289672; PMID:1600940		
A:Accession: S22696		
A:Molecule type: mRNA		
A:Residues: 1-365 <VER>		
A:Cross-references: UNIPROT:P45986; UNIPARC:UPI000012D637; EMBL:		
R:Rammesmayr, G.; Pichorner, H.; Adams, P.; Jensen, R.G.; Bohne		
Arch. Biochem. Biophys. 322, 183-188, 1995		
A:Title: Characterization of IMT1, myo-inositol O-methyltransfer		
A:Reference number: S66386; MUID:9600494; PMID:7574673		
A:Contents: annotation		
C:Genetics:		
A:Gene: Imt1		
C:Superfamily: O-methyltransferase		
C:Keywords: methyltransferase; S-adenosylmethionine; stress-indu		
Query Match		
Best Local Similarity 54.3%; Pred. No. 3e-78;		
Matches 190; Conservative 70; Mismatches 88; Indels		
Qy	18 EEEAFVPMQLTSASVLPVYLKSAIELDVLEIMAKAGCAHISTDIASK	AV 77
Db	18 DEQLAGLAVTLANMAAFMILKSAFELKILDIIFSAGSGVSVSTSEISQ	PV 77
Qy	78 MLDRMLRLIASYSVLTCSLRTLDPDKIERLYGLAPVCKFLTRNDGVSA	KV 137
Db	78 ILDRMLRLIASHSVLTCLQK-GECSGQRYVGPAPLCNYLASNDGQSLG	KV 136
Qy	138 LMESWYHLTEAVLEGIPFKKAYGMTAFEHGTDPRFTVPFNNGMSNST	TY 197
Db	137 MMSWFLNDYILEGGVFPKRAHGMIOFDYGTDBRFNHFVNOGAAHTI	NY 196
Qy	198 KGFEGLSVVDVGSGTAHLMITIAKYPMIGINDELPHVIEBAPSYGV	VS 257
Db	197 NGFNDYKVLVDVGNGIGVNGMIVAKTHIKGINVDLPHVITADAPSYGV	ES 256
Qy	258 VPKGDALFMKWLCHDMSDEHCLKFLKKCYEALPTNGKYLAECLIPVAD	VH 317
Db	257 IPQADALFMKWLHDMSDHCLKFLKKCYESLAKGKITLVESLIPVPE	FS 316
Qy	318 IDVIMLANHPGKERTKEFEALAKGAFEGPRVVASCAVNTWIIIEFLKX	

NID:g167261; PIDR

ulative halophyt

004

CN 357

VR 118

VF 178

VF 178

VI 238

VI 238

LA 298

VV 298

YN 358

VF 178

VF 178

FS 316

Db 317 LDCHLVNNGGKERSKEDFALASKTGSTVDVLC-CAYDTWWEIYK 365

RESULT 12

T09617

Isoiquiritigenin 2'-O-methyltransferase - alfalfa

C:Species: Medicago sativa (alfalfa)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #next_change 09-Jul-2004

C:Accession: T09617

R:Maxwell, C.A.; Harrison, M.J.; Dixon, R.A.

Plant J. 4, 971-981, 1993

A:Title: Molecular characterization and expression of alfalfa isoiquiritigenin 2'-O-methyltransferase.

A:Reference number: 216778; MUID:94108491; PMID:8281189

A:Accession: T09617

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-372 <MAX>

A:Cross-references: UNIPROT:P93324; UNIPARC:UPI000000A3969; EMBL:LI0211; NID:g289126; PID

A:Experimental source: subspecies sativa; cultivar Apollo

C:Function:

A:Description: methylates the 2'-hydroxyl of isoiquiritigenin (2',4',4'-trihydroxychalcone)

A:Note: 4',4'-dihydroxy-2'-methoxychalcone is the most potent of the nod-gene-inducing flavonoids

C:Superfamily: O-methyltransferase

C:Keywords: methyltransferase

Query Match 43.7%; Score 836; DB 2; Length 372;

Best Local Similarity 46.9%; Pred. No. 6, 7e-61;

Matches 175; Conservative 71; Mismatches 119; Indels 8; Gaps 5;

```

1 MGS---TSEFKSPSEAAAEAFVFAVQLTSASVLPWVLSKATLEDTLEIMAKG-GRG 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MGNSTTTEDNDNISATSEGTEDSACLSAMVLTNNVLPVAVLAALDNLFEIIAAKATPPG 60

57 AHSSTDIASKLP--TKNPDAVMDRLRLILASYSVLTCSLRTLPDGKIERLYGLAPVC 114
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 AFMSPEIASKLPASTQSHDLFNRDLRLILASYSVLTCSLRTLEDGAEKRVYGLSVMVG 120

115 KFLTRNDGVSIALSLNQDKVLMESWHLTEAVLEGGIP-FNKAYGMTAEFGHTDPR 173
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 KVLVDESNGYLDASTFLCYPALQLQVNNMFKEAVVDEDIDLFKNVHGVTKEFNGKXK 180

174 FNTVFNNGSNHSTTMMKILFTYKGFEGSLGVVDVGGGTGAHLMITAKYPMKGINPD 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 MNOIRNKSWVDCAETKMKMLITYGEGISTLVDDGGSGKNLEIILISKYPLKGINPD 240

234 LPHVIEAPSPGVHVGDMFVSVPKDAIPMKWICHMSDEHCLKFLKKCYEALPTNG 293
241 LPOVIENAPPLSGIEHVGDMFASVQDGAMITKAVCHMSDEKCIIEFLSNCHKALSPNG 300

294 KYTLAECLIPVAPDASLPKTAVNHIDVIMLANNPGKERTKEFEFLAKAGAFEGPRVVA 353
301 KYIIVEFLIPPEPNPSESKVLSTLDNMF-TVGGRETERKQYEXTKLGSFKFQVAC 359

354 SCAYNTWIIIEFLK 366
360 RAFNSLGWIEFYK 372

```

RESULT 13

E96559

hypothenical protein P5F19.5 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #next_change 09-Jul-2004

C:Accession: E96559

R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arab

A:Reference number: A66141; MUID:21016719; PMID:11130712

A:Accession: E96559

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-363 <STO>

A:Cross-references: UNIPROT:Q9ZU24; UNIPARC:UPI0000048381; GB:AE

C:Genetics:

A:Gene: P5F19.5

A:Map position: 1

C:Superfamily: O-methyltransferase

Query Match 43.4%; Score 832; DB 2; Length 363;

Best Local Similarity 47.3%; Pred. No. 1.4e-60;

Matches 168; Conservative 64; Mismatches 119; Indels

```

12 SEAAAEAEAFVFAVQLTSASVLPWVLSKATLEDTLEIMAKGAP-GAHIS'
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 TSGGSEEDMLAIQLGSLNFVPIYVKTARELDLFEIMAKARPISYLSI

71 KNPDAAVMDRLRLILASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTRNI
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
66 KNPHAPMIMIDRLFLVAVSVCTKLVDEBGRSRAVGLGVGCKLTKD

131 LMNDKVLMESSMYHLTEAVLEGGI-FNKAYGMTAEFGHTDPRNTFNI
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
126 LAGCTKAGVWSYVTEITQEGASAWERANBALIFEMKKNENLKKLFNI

190 MKKILFTYKGFEGSLGVVDVGGGTGAHLMITAKYPMKGINFDPVHVEI
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
186 MKKILENVIIGFEGVSDPVDVGSLGSLNLAQLISKVPHIKGINFDPVHVKD

250 VGDMPFVSVPKGDALPMKWICHMSDEHCLKFLKKCYEALPTNGKVIILAEK
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
246 IGGWIFDEIPRGEVILMKMIIHNDKCVBLIKKCKALPBTGRIIVIER

309 SLPTKAVVHIDVIMLANNPGKERTKEFEFLAKAGAFEGPRVVASCAVN
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 DLATKNSLSADLTWMSLTSGGKERTKEFEFLAKAGAFKLPKTIYV-GAYS

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RESULT 14

G96804

hypothenical protein TSM16.12 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #next_change

C:Accession: G96804

R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Jensen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arab

A:Reference number: A66141; MUID:21016719; PMID:11130712

A:Accession: G96804

A:Status: preliminary

A:Molecule type: DNA

A:Gene: P5F19.5

A:Map position: 1

C:Superfamily: O-methyltransferase

Query Match 43.4%; Score 831.5; DB 2; Length 38;

Best Local Similarity 45.6%; Pred. No. 1.6e-60;

Matches 171; Conservative 72; Mismatches 113; Indels

un, H.; Tallon, I

ID:g4220447; PII

70

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65

130

125

189

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QY 2 GSTSETKMSPSSEAAAEEBAFVPMQUTSASVLPMLKSAIELDVLEIMAKAGPGAHIST 61
DB 16 GLTKEQEIDEKQVSLQAESIV-----NAVAFPMVLKALLEGVIDTIAAASNGTMLS 69
QY 62 SDIASLPTK--NPDAAVMLDRLMLRLIASVYLTC-----SLRTLPGDKIERLYGLAPVCK 115
DB 70 SEIANSLEPKFPNPEAPVLLDRLMLRLVSHSLIKCCMVESRENGQTKIERVYAAEPICK 129
QY 116 FLTRNDGV-SIALSLMNQDKVLMSWYHLTEAVLEGGIPFNKAYGMAFEXHGTDPFR 174
DB 130 YELKSDSGSGSLSSILLHLSQVILKTNLKVLEGGKAFSSANDMLFETISDDDF 189
QY 175 NTVPNNGNSNHTITMKLLETYYKGFEGSGSVYDGGCGAHLMNTIATYPMIKGINFPL 234
DB 190 SKLFRRAMESSTTMMKVLVEERGFEDVNTLVGGGIGTILGLITSKYPIHKGVNFDL 249
QY 225 PHVIEBAPSPGVENHVGDMFVSPKGDALFMKWIChMSDEHCLFKKCYEALPTNGK 294
DB 250 AOVLTQAPFPYGVKXVSGDMFIEVPKGDALFMKWIHDGDEDCIKILNCKMSLPECKG 309
QY 295 VILAECLIPVAP--DASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAFEGFRV 351
DB 310 VIVEMITPMERKXPNDFGNT--VLGMDLMLTQCSGGKERSLSQFENLAFASGFLCEI 367
QY 352 VASCAVNTWITIEFLK 366
DB 368 IC-LSYSYSVIEFHK 381

RESULT 15

P96804
Hypothetical protein TSM16.11 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96804
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chih, C.W.; Chung, M.K.; Comu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Author: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: F96804
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-381 <STO>
A:Cross-references: UNIPROT:Q9CA04; UNIPARC:UPI00000484A1; GB:AE005173; NID:g6382499; P
C:Genetics:
A:Gene: TSM16.11
A:Map position: 1
C:Superfamily: O-methyltransferase

Query Match 43.4%; Score 830.5; DB 2; Length 381;
Best Local Similarity 45.5%; Pred. No. 28-60;
Matches 168; Conservative 64; Mismatches 122; Indels 15; Gaps 6;
QY 9 MSPSEAAAEEBAFVPMQUTSASVLPMLKSAIELDVLEIMAKAGPGAHISTSDIASKL 68
DB 17 LTKEQEVDEKQVSLQAESIVNTVAFPMVLKALLEGVIDTIAAASNDTMLSPCRISCSL 76
QY 69 PTK--NPDAAVMLDRLMLRLIASVYLTC-----RTLPGDKIERLYGLAPVCKFLTR 119
DB 77 PTKPFPNPEAPVLLDRLMLRLVSHSLIKCKMITGEGKRT--GKIERVYAAEPVCKYFLR 133
QY 120 NDDGV-SIALSLMNQDKVLMSWYHLTEAVLEGGIPFNKAYGMAFEXHGTDPFRNTVF 178
DB 134 DSDGTGSLVPLFMFLHTQVFFKTNLKVLEGGKAFSSANDMLFETISDDDF 193

QY 179 NNGMSNHTITMKLLETYYKGFEGSGSVYDGGCGAHLMNTIATYPMIK 238
DB 194 NRAMSEPTMIMKXVLDVVRGFEDVNTLVGGGIGTILGLITSKYPIHK 253
QY 239 BEAPSPGVENHVGDMFVSPKGDALFMKWIChMSDEHCLFKKCYEA 298
DB 254 TQAPFPYGVENHVGDMFIEVPKGDALFMKWIHDGDEDCIKILNCKMS 313
QY 299 ECLIPVAP-DASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKGAF 357
DB 314 EFVTPKEPKGDLSSNTVAFMDLMLTQCSGGKERSLSQFENLAFASGFL 372
QY 358 NTWITIEFLK 366
DB 373 SYSVIEFHK 381

Search completed: December 12, 2005, 08:38:10
Job time : 42 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSs have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 08:26:54 / Search time 230 Seconds
(without alignment)
1128.845 Million cell updates/sec

Title: US-10-681-878A-6
Perfect score: 1915
Sequence: 1 MGSTSETKMSPEAAAAEE.....FRVASCANNTWTFLEKKI 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 05.80:*
1: uniprot_prot:*
2: uniprot_trendi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894.5	98.9	367	09SMR0_LIOST	09SMR0 liquidambar
2	1602.5	83.7	365	1 COMT1_FRUDU	043609 prunus dulc
3	1601.5	83.6	365	1 COMT1_ROSCH	089125 rosa chinen
4	1595.5	83.3	365	1 COMT1_POPPM	000763 populus tre
5	1595.5	83.3	365	2 07X9J0_ROSCH	07X9J0 rosa chinen
6	1589.5	83.0	365	2 09M602_FRAN	09M602 fragaria an
7	1588.5	83.0	365	1 COMT1_FOPKI	043046 populus kit
8	1579.5	82.5	360	2 09M565_9ROSI	09M565 populus tom
9	1578.5	82.4	364	1 COMT1_MEDSA	091W88 populus tri
10	1544.5	80.7	365	1 COMT1_MEDSA	P28002 medicago sa
11	1535	80.2	366	1 COMT1_EUCGL	P46484 eucalyptus
12	1528	79.8	370	1 COMT1_CLABR	023760 clarkia bre
13	1523.5	79.8	359	1 COMT1_CAPAN	09FY88 capsicum an
14	1523.5	79.6	361	1 COMT1_LOCIA	09XG40 ocimum basi
15	1511	78.9	364	1 COMT3_POPKI	043047 populus tre
16	1510	78.9	364	1 COMT2_POPPM	041086 populus tre
17	1506.5	78.7	363	1 COMT1_CATRO	08W013 catharanthu
18	1499.5	78.3	364	2 042958_TOBAC	042958 nicotiana t
19	1491.5	77.9	361	1 COMT2_TOBAC	09XG95 ocimum basi
20	1484.5	77.5	364	2 004065_TOBAC	004065 nicotiana t
21	1483.5	77.5	350	1 COMT1_COFCA	081187 coffea cane
22	1473.5	76.9	363	1 COMT1_ARATH	09FX25 arabidopsis
23	1468.5	76.7	359	1 COMT1_CAPCH	081646 capsicum ch
24	1460.5	76.3	365	2 06T1F5_PAPIA	06T1F5 annel majus
25	1432	74.8	386	2 09M560_VITVI	09M560 vitis vinif
26	1403.5	73.3	350	2 06S362_MESCR	06S362 mesembryant
27	1401	73.2	362	2 09X890_USRUD	09X890 thalictrum
28	1395	72.8	362	2 09S9Y9_USRUD	09S9Y9 thalictrum
29	1395	72.8	362	2 09X892_USRUD	09X892 thalictrum
30	1389	72.5	364	2 09S9Y8_USRUD	09S9Y8 thalictrum
31	1387	72.4	343	1 OMT2_CHRAE	042653 chrysosplen

32	1384	72.3	312	2	09SMC1_EUCGL	09SMC1	ptus
33	1384	72.3	364	2	09X891_USRUD	09X891	trum
34	1383	72.2	343	1	OMT1_CHRAE	P5904	splen
35	1341	70.0	368	1	1EMT1_CLABR	00438	a bre
36	1329	69.4	354	1	COMT1_ZINEL	04323	eleg
37	1266.5	66.1	360	2	06WUC0_PAPSO	06WUC0	r som
38	1266	65.1	313	1	COMT1_EUCGL	09SMC1	ptus
39	1246	65.1	360	2	094GA5_PESAR	094GA5	a aru
40	1246	65.0	360	2	094GA8_PESAR	094GA8	a aru
41	1241	64.8	360	2	022381_LOLPR	02238	pere
42	1239	64.7	360	2	084N28_WHEAT	084N28	um ae
43	1234	64.4	360	2	092TU2_LOLPR	092TU2	. pere
44	1234	64.4	360	2	COMT1_SACOF	08205	rum o
45	1213	63.3	362	1	092TU0_LOLPR	092TU0	pere
46	1212.5	63.3	361	2	06UNM7_9POAL	06UNM7	rum h
47	1212	63.3	362	2	05KSL8_IRIHO	05KSL8	ollan
48	1208.5	63.1	365	2	094GA7_PESAR	094GA7	a aru
49	1207	63.0	360	2	042654_CHRAE	04265	splen
50	1198	62.6	343	2	06ZD89_ORYSA	06ZD89	sativ
51	1194	62.3	368	2	06WMP7_MAIZE	06WMP7	ys (m
52	1193	62.3	364	2	06T1F6_PAPIA	06T1F6	ajub.
53	1191.5	62.2	354	2	06VMB6_MAIZE	06VMB6	ys (m
54	1187	62.0	364	2	COMT1_MAIZE	00650	ys (m
55	1185	61.9	364	1	06GLJ5_MAIZE	05GLJ5	ys (m
56	1185	61.9	364	2	06VMB3_MAIZE	06VMB3	ys (m
57	1184	61.8	364	2	06VMB5_MAIZE	06VMB5	ys (m
58	1184	61.8	364	2	06VMB2_MAIZE	06VMB2	ys (m
59	1172	61.2	358	2	06VMB2_MAIZE	06VMB2	ys (m
60	1164	60.8	359	2	06VMB6_MAIZE	06VMB6	ys (m
61	1164	60.8	359	2	06VMB5_MAIZE	06VMB5	ys (m
62	1164	60.8	359	2	06VMB8_MAIZE	06VMB8	ys (m
63	1163	60.7	358	2	06VMB3_MAIZE	06VMB3	ys (m
64	1163	60.7	359	2	06VMB2_MAIZE	06VMB2	ys (m
65	1163	60.7	359	2	06VMB2_MAIZE	06VMB2	ys (m
66	1162	60.7	358	2	06VMB1_MAIZE	06VMB1	ys (m
67	1152	60.2	362	2	084X55_SORBI	084X55	m bic
68	1147	59.9	362	2	08W215_SORBI	08W215	m bic
69	1142.5	59.7	371	2	06L8K4_ROSCH	06L8K4	hinen
70	1135	59.3	364	2	05NDD5_PICAB	05NDD5	abies
71	1090.5	56.9	365	2	06Q796_VANPL	06Q796	a pla
72	1064.5	55.6	364	2	06VMV9_MENPI	06VMV9	pide
73	1062.5	55.5	365	2	042949_TOBAC	042949	ana t
74	1059	55.3	292	2	070CS6_PESAR	070CS6	a aru
75	1047	54.7	365	1	1MT1_MESCR	P4598	tyanc
76	1046	54.6	292	2	070CS7_LOLMU	070CS7	mult
77	1037	54.2	364	2	08S3K6_TOBAC	08S3K6	ana t
78	978	51.1	351	2	092TU1_LOLPR	092TU1	Q92TU
79	975	50.9	268	2	075W57_ORYSA	075W57	sativ
80	948.5	49.5	352	2	08H0D1_HORVU	08H0D1	m vul
81	910	47.5	366	2	07X9J0_ROSCH	07X9J0	hinen
82	836	43.7	372	1	CHOMT1_MEDSA	P9332	go sa
83	832	43.4	363	2	09ZU24_ARATH	09ZU24	opsis
84	831.5	43.4	381	2	09CAQ3_ARATH	09CAQ3	opsis
85	830.5	43.4	381	2	09CAQ4_ARATH	09CAQ4	opsis
86	824.5	43.1	381	2	084WU8_ARATH	084WU8	opsis
87	824	43.0	367	2	096424_GLYEC	096424	opsis
88	817.5	42.7	368	2	08BLAK_ARATH	08BLAK	opsis
89	811.5	42.4	352	2	09WAP0_ARATH	09WAP0	opsis
90	805	42.0	201	2	071H66_WHEAT	071H66	um ae
91	803.5	42.0	373	2	09LPU8_ARATH	09LPU8	opsis
92	797	41.6	381	2	SMT1_COPUA	03552	opsis
93	794.5	41.5	373	2	09LPU5_ARATH	09LPU5	japo
94	793.5	41.4	373	2	056XW7_ARATH	056XW7	opsis
95	790.5	41.3	373	2	08LGI0_ARATH	08LGI0	opsis
96	789.5	41.3	373	2	09LPU7_ARATH	09LPU7	opsis
97	789.5	41.2	373	2	09LPU6_ARATH	09LPU6	opsis
98	788	41.1	378	2	0818L1_ARATH	0818L1	opsis
99	787	41.1	378	2	09PHZ5_ARATH	09PHZ5	opsis
100	780.5	40.8	381	2	09CAM5_ARATH	09CAM5	opsis

ALIGNMENTS

```

RESULT 1
Q9SWR0 LIQST PRELIMINARY; PRT; 367 AA.
ID Q9SWR0;
AC Q9SWR0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Caffeate O-methyltransferase (EC 2.1.1.6).
GN Caffeate O-methyltransferase
OS Name:COMT;
OS Liquidambar styraciflua (Amberboom) (Sweetgum tree).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Hamamelidaceae; Liquidambar.
OX NCBI_TaxID=4400;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Developing xylem;
RX MEDLINE=99362692; PubMed=10430877; DOI=10.1073/pnas.96.16.8955;
RA Osakebe K., Tsao C.C., Li L., Popko J.L., Umezawa T., Carraway D.T.,
RA Smeltzer R.H., Joshi C.P., Chiang V.L.;
RT "Conferyl aldehyde 5-hydroxylation and methylation direct syringyl
RT lignin biosynthesis in angiosperms."
RL Proc. Natl. Acad. Sci. U.S.A. 96:8955-8960(1999).
DR EMBL; AF139533; AAD48913.1; -, mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q9SWR0; 7-367.
DR GO; GO:0016206; F:catechol O-methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00891; Methyltransf_2; 1.
DR Methyltransferase; Transferase.
KW SEQUENCE 367 AA; 39970 MW; 3F05B9BCB711779 CRC64;
SQ
Query Match 98.9%; Score 1894.5; DB 2; Length 367;
Best Local Similarity 99.5%; Pred. No. 1,9e-141;
Matches 366; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGSTSETKNSPSEAAAAEEBAFVFMQLTSASVLPMTLSAIEDVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKNSPSEAAAAEEBAFVFMQLTSASVLPMTLSAIEDVLEIMAKAGPGAHIS 60
QY 61 TSDIASKLPTKNPDAVMDRLRLASYSVLTCSLRTPDQKIERLYGLAPVCKELTEN 120
DB 61 TSDIASKLPTKNPDAVMDRLRLASYSVLTCSLRTPDQKIERLYGLAPVCKELTEN 120
QY 121 DGVSAIALSLNNQDVKLVMSWYHLTEAVLEGGIPFNKAYGWTAFEYHGTDPRENTVPFN 180
DB 121 DGVSAIALSLNNQDVKLVMSWYHLTEAVLEGGIPFNKAYGWTAFEYHGTDPRENTVPFN 180
QY 181 GMSNHSITTMKKILETYGFGELGSVVDVGGTGALNNMIIAKYPMIKGINFDLPVIEE 240
DB 181 GMSNHSITTMKKILETYGFGELGSVVDVGGTGALNNMIIAKYPMIKGINFDLPVIEE 240
QY 241 AASYGVHEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYLALAC 300
DB 241 AASYGVHEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYLALAC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPEGRVVAACAINTM 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPEGRVVAACAINTM 360
QY 361 IIEFLKKI 368
DB 361 IIEFLKKI 367

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AC Q43609;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl
DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM
GN Name:COMT1;
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC rosids; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunu
OX NCBI_TaxID=3755;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=cv, Texas; TISSUE=Root;
RA Garcia-Mas J., Messager R., Arus P., Puigdomenech P.;
RT "The caffeic acid O-methyltransferase from Prunus amygdalus
RL (ex) Plant Gene Register PGR95-006.
CC CC
CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to fi
CC and of 5-hydroxyferulic acid to sinapic acid. The resulti
CC products may subsequently be converted to the correspon
CC alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihyd
CC cinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hyd
CC cinamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily;
CC family. COMT subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through
CC between the Swiss Institute of Bioinformatics and the Emi
CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this st
CC removed.
CC -----
DR EMBL; X83217; CAA58218.1; -, mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q43609; 5-364.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF08100; Dimerisation; 1.
DR Pfam; PF00891; Methyltransf_2; 1.
DR Lignin biosynthesis; Methyltransferase; Transferase.
KW SEQUENCE 365 AA; 39762 MW; C8C4BFE7E0180E7 CRC64;
SQ
Query Match 83.7%; Score 1602.5; DB 1; Length 31
Best Local Similarity 82.8%; Pred. No. 2,5e-118;
Matches 304; Conservative 31; Mismatches 29; Indels
QY 1 MGSTSETKNSPSEAAAAEEBAFVFMQLTSASVLPMTLSAIEDVLEIMAKAGPGAHIS 60
DB 1 MGSTSETKNSPSEAAAAEEBAFVFMQLTSASVLPMTLSAIEDVLEIMAKAGPGAHIS 60
QY 61 TSDIASKLPTKNPDAVMDRLRLASYSVLTCSLRTPDQKIERLYGLAPVCKELTEN 120
DB 61 TSDIASKLPTKNPDAVMDRLRLASYSVLTCSLRTPDQKIERLYGLAPVCKELTEN 120
QY 121 DGVSAIALSLNNQDVKLVMSWYHLTEAVLEGGIPFNKAYGWTAFEYHGTDPRENTVPFN 180
DB 121 DGVSAIALSLNNQDVKLVMSWYHLTEAVLEGGIPFNKAYGWTAFEYHGTDPRENTVPFN 180
QY 181 GMSNHSITTMKKILETYGFGELGSVVDVGGTGALNNMIIAKYPMIKGINFDLPVIEE 240
DB 181 GMSNHSITTMKKILETYGFGELGSVVDVGGTGALNNMIIAKYPMIKGINFDLPVIEE 240
QY 241 AASYGVHEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYLALAC 300
DB 241 AASYGVHEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGKYLALAC 300
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPEGRVVAACAINTM 360
DB 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGGKERTKEFEALAKAGPEGRVVAACAINTM 360

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Db      229 ILVAPDSSLATKGVVHIDVIMLANHGGKERTEDQFQALAGAGGFGNVAACS-AFNTY 357
QY      361 IIEFLKK 367
Db      358 VIEFLKK 364

RESULT 3
COMT1 ROSCH STANDARD; PRT; 365 AA.
AC      08GU25;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-
GN      methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
OS      Rosa chinensis (China rose).
OC      Burkariya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC      rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OX      NCBI_TaxId=74649;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=cv. Old Blush;
RA      Cock J.M., Scalliet G., Huguency P.;
RT      "Characterisation of a novel O-methyltransferase involved in the
RT      biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two
RT      major scent components of rose flowers.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC      and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC      products may subsequently be converted to the corresponding
CC      alcohols that are incorporated into lignins.
CC      -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC      cinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC      cinamate.
CC      -1- PATHWAY: Lignin biosynthesis.
CC      -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC      family. COMT subfamily.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AJ439740; CAD29457.1; -; mRNA.
DR      HSSP; P28002; 1K1Z.
DR      SMR; Q8GU25; 5-365.
DR      InterPro; IPR012967; Dimerisation.
DR      InterPro; IPR001601; Methyltransf.
DR      InterPro; IPR001077; O Met. trans2.
DR      InterPro; IPR000051; SAM_bdt.
DR      InterPro; IPR011991; Wing_hlx_DNA_bd.
DR      Pfam; PF08100; Dimerisation_1.
DR      Pfam; PF00891; Methyltransf_2; 1.
DR      KEGG; Lignin biosynthesis; Methyltransferase; Transferase.
SQ      SEQUENCE 365 AA; 39727 MW; CJS4528559B64358 CR664;

Query Match 83.6%; Score 1601.5; DB 1; Length 365,
Best Local Similarity 81.5%; Pred. No. 36-118;
Matches 300; Conservative 38; Mismatches 27; Indels 3; Gaps 2;

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QY      121 DGVSIATSLMNQKVTLMESWYHLTEAVLEGIPPNKAYGNTATERYHGT
DB      119 EDGVSIATSLMNQKVTLMESWYHLTEAVLEGIPPNKAYGNTATERYHGT
QY      181 GMSNSTITMKKILETFYGGFEGLSVVDVGGGTGAHLMNIIMKYPIMKGI
DB      179 GMADSTITMKKILETFYGGFEGLSVVDVGGGTGAHLMNIIMKYPIMKGI
QY      241 ABSYPGEHVGGDMFVSVPKGDALFMKWIICHDMSDEHCLKFLKKCYEALF
DB      239 APOYPGVGVGGDMFVSVPKGDALFMKWIICHDMSDEHCLKFLKKCYEALF
QY      301 ILVAPDSSLATKGVVHIDVIMLANHGGKERTEDQFQALAGAGGFGNVAACS-AFNTY 357
DB      299 ILVAPDSSLATKGVVHIDVIMLANHGGKERTEDQFQALAGAGGFGNVAACS-AFNTY 357
QY      361 IIEFLKKI 368
DB      358 VIEFLKKI 365

RESULT 4
COMT1 POPTM STANDARD; PRT; 365 AA.
AC      000763; Q43094;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-
GN      methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (
OS      Populus tremuloides (Quaking aspen).
OC      Burkariya; Viridiplantae; Streptophyta; Embryophyta; Trache
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC      rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Pop
OX      NCBI_TaxId=3693;
RN      [1]
RP      NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 165-184; 335-3
RP      349-359.
RC      TISSUE=xylem;
RA      MEDLINE=92032785; PubMed=1932694;
RT      "cDNA cloning, sequence analysis and seasonal expression of
RT      a specific caffeic acid/5-hydroxyferulic acid O-methyltrans
RT      aspen.";
RL      Plant Mol. Biol. 17:1203-1215 (1991).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      MEDLINE=95288573; PubMed=7770534; DOI=10.1104/pp.107.4.1459
RA      Teal C.-J., Podila G.K., Chiang V.L.C.;
RT      "Nucleotide sequence of a Populus tremuloides gene encoding
RT      caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
RL      Plant Physiol. 107:1459-1459 (1995).
RN      [3]
RP      SEQUENCE REVISION.
RA      Teal C.-J., Mielke M.R., Podila G.K., Chiang V.L.C.;
RL      Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      PROTEIN SEQUENCE OF 165-184; 335-346 AND 349-359.
RC      TISSUE=xylem;
RA      MEDLINE=92344802; PubMed=1368360; DOI=10.1016/0031-9422(92)
RA      Bugos R.C., Chiang V.L., Campbell W.H.;
RT      "Characterization of a Populus tremuloides gene encoding
RT      methyltransferase from aspen.";
RL      Phytochemistry 31:1495-1498 (1992).
CC      -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
CC      and of 5-hydroxyferulic acid to sinapic acid. The resul
CC      products may subsequently be converted to the correspon
CC      alcohols that are incorporated into lignins.
CC      -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihyd
CC      cinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hyd
CC      -----
CC      -1- PATHWAY: Lignin biosynthesis.

```

CC -1- TISSUE SPECIFICITY: Xylem.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2 family. COYT subfamily.
 CC -----
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; X62036; CA444006.1; -; mRNA.
 CC EMBL; U13171; AAB61731.1; -; Genomic_DNA.
 CC PIR; S18568; S18568.
 CC HSSP; P28002; 1KYZ.
 CC SMR; Q00763; 5-364.
 CC InterPro; IPR012967; Dimerization.
 CC InterPro; IPR001601; Methyltransf.
 CC InterPro; IPR001077; O_Met_trans2.
 CC InterPro; IPR000051; SAM_bd.
 CC InterPro; IPR011991; Wing_hlx_DNA_bd.
 CC Pfam; PF08100; Dimerization_1.
 CC Pfam; PF00891; Methyltransf_2; 1.
 CC Direct protein sequencing; High in biosynthesis; Methyltransferase;
 CC Transference.
 SQ SEQUENCE 365 AA; 39805 MW; A6CECDBA4E0007CD CRC64;

Query Match 83.3%; Score 1595.5; DB 1; Length 365;
 Best Local Similarity 80.9%; Pred. No. 8.9e-118;
 Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSSTETKSPSEAAAEAFVPMQUTSASVLPVMTLSAIELDVLEIMAKAGAHIS 60
 DB 1 MGSSTETQMTPTQ--VSDEAHIFAMQLASASVLPMTLTAIELDLEIMAKAGAHIS 58
 QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGLAVCKEFLTN 120
 DB 59 TSEIASHLPTKQPDAAVMDRLRLRLASYSILTCSKDPDGKVERLYGLAVCKEFLTN 118
 QY 121 DDGVSIALSLMNOQKLVESWYHLTEAVLEGGIIPFNKAYGWTAFEGHDTDRFNTVFN 180
 DB 119 EDGVSIALSLMNOQKLVESWYHLTEAVLEGGIIPFNKAYGWTAFEGHDTDRFNTVFN 178
 QY 181 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPIMIKINFDLPVIE 240
 DB 179 GMSDSTITMKKILETYGFEGLGSVVDVGGGTGAHVNTIVSKYPIKINFDLPVIED 238
 QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPTNGXYILAEC 300
 DB 239 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDAHCLKFLKNCYDALPENGXYILVBC 298
 QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGRKERTKFEFLAKGAGEGRRVVASCAVNTW 360
 DB 299 ILPVAPDTSLATKGVVHIDVIMLAHNPGRKERTKFEFLAKGAGQGFQFVNC-CAFNTH 357
 QY 361 IIEFLKK 367
 DB 358 VIEFLKK 364

RESULT 5
 Q7X9J0 ROSCH PRELIMINARY; PRT; 365 AA.
 AC Q7X9J0;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Caffeic acid O-methyltransferase.
 GN Name=RCOMT2;
 OS Rosa chinensis var. spontanea.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosida I; Rosales; Rosaceae; Rosoideae; Rosa.

OX NCBI_TaxID=197613;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Rose flower petals;
 RC Wu S., Watanabe N., Mita S., Ueda Y., Shibuya M., Ebizuka Y
 RA "Two O-methyltransferases isolated from flower petals of Ros
 RT chinensis var. spontanea involved in scent biosynthesis.",
 RL J. BioSci. Bioeng. 0:0-0(2003).
 DR EMBL; AB086104; BAC78827.1; -; mRNA.
 DR HSSP; P93324; 1FP1.
 DR SMR; Q7X9J0; 5-365.
 DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltran
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009809; P:Lignin biosynthesis; IEA.
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR001077; O_Met_trans2.
 DR InterPro; IPR000051; SAM_bind.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF00891; Methyltransf_2; 1.
 DR Methyltransferase; Transference.
 SQ SEQUENCE 365 AA; 39669 MW; 2846D4B039B65A70 CRC64;

Query Match 83.3%; Score 1595.5; DB 2; Length 36
 Best Local Similarity 81.5%; Pred. No. 8.9e-118;
 Matches 300; Conservative 37; Mismatches 28; Indels

QY 1 MGSSTETKSPSEAAAEAFVPMQUTSASVLPVMTLSAIELDVLEIM 1S 60
 DB 1 MGSSTETQMTPTQ--VSDEAHIFAMQLASASVLPMTLTAIELDLEIM JS 58
 QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASYSVLTCSLRTLPDGKIERLYGL IN 120
 DB 59 PNDLASQLPTKQPDAAVMDRLRLRLASYSILTCSKDPDGKVERLYGL CN 118
 QY 121 DDGVSIALSLMNOQKLVESWYHLTEAVLEGGIIPFNKAYGWTAFEGHT IN 180
 DB 119 EDGVSIALSLMNOQKLVESWYHLTEAVLEGGIIPFNKAYGWTAFEGHT JK 178
 QY 181 GMSNSTITMKKILETYGFEGLGSVVDVGGGTGAHLNMIIAKYPIMIGI IN 240
 DB 179 GMSDSTITMKKILETYGFEGLGSVVDVGGGTGAHVNTIVSKYPIKIN IN 238
 QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALP IC 300
 DB 239 APQYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKNCYALP IC 298
 QY 301 ILPVAPDASLPTKAVVHIDVIMLAHNPGRKERTKFEFLAKGAGFEGRI IW 360
 DB 299 ILPVAPDTSLATKGVVHIDVIMLAHNPGRKERTKFEFLAKGAGFQIRI Y 357
 QY 361 IIEFLKKI 368
 DB 358 VIEFLKKI 365

RESULT 6
 Q9M602 PRAAN PRELIMINARY; PRT; 365 AA.
 ID Q9M602;
 AC Q9M602;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE O-methyltransferase.
 GN Name=omt1;
 OS Fragaria ananassa (Strawberry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots
 OC eurosida I; Rosales; Rosaceae; Rosoideae; Fragaria.
 OX NCBI_TaxID=3747;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kaldenhoff R., Wein M., Schwab W.;

Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB220491; AAF28353.1; -, mRNA.
DR HSSP; P28002; 1K1Z.
DR SMR; Q9M602; 5-365.
DR GO; GO:0008171; P:O-methyltransferase activity; IEA.
DR GO; GO:0008175; P:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR InterPro; IPR001601; Methyltransferase.
DR InterPro; IPR001077; O_Mec_transf.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00891; Methyltransferase_2; 1.
DR Methyltransferase; Transferase.
SQ SEQUENCE 365 AA; 39817 MW; EF748F753E55B0CB CRC64;

Query Match 83.0%; Score 1589.5; DB 2; Length 365;
Best Local Similarity 81.0%; Pred. No. 2,7e-117;
Matches 298; Conservative 39; Mismatches 28; Indels 3; Gaps 2;

QY 1 MGSSTETKMSPEBAABEAEAFVPMQLTSAVLPVMTKSAIEDVLEIMAKAGPGAHIS 60
DB 1 MGSSTETQMTPTQH--VSDEEAMLFAMQLASASVLPVMTKSAIELEIMAKAGPGSFLS 58

QY 61 TSDIASKLPTKQPDAAVMDRLRLASYSVLTCSRLTPDGKIRLRYGLAPVCKELTEN 120
DB 59 PBDLASQLPTKQPDAAVMDRLRLASYSILTCSRLTPDGKIRLRYGLAPVCKELTEN 118

QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGMTAFEPHYGTDPRFNTFNN 180
DB 119 EDGVSIALCLNODKVLMSWYHLKDVAIDGSIPTNKAYGMTAFPHYGTDRFNNVFK 178

QY 181 GMSNSTITMKKILETTYKGFEGISVVDYGGGTGAHLNMIITAKYPMIKINFDLPVIEE 240
DB 179 GMSNSTITMKKILETTYKGFEGIKSVVDYGGGTGAHVNMIVSKYPSIKINFDLPVIED 238

QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKYLIAEC 300
DB 239 APQYGEVHGDMFVSVPKGNALFMKWI CHDMSDEHCLKFLKCCYEALPDGKYLIAEC 298

QY 301 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFRVVASCAVNTW 360
DB 299 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGSGRQGRVCCD-AFNTY 357

QY 361 IIEFLKKI 368
DB 358 VIEFLKKI 365

RESULT 7
COMTI_POPKI STANDARD; PRT; 365 AA.
AC Q43046;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (CAOMT-1). Name=HOMT1;
OS Populus kitchamiensis (Aspen).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
NCBI_TaxId=3698;
RN NUCLEOTIDE SEQUENCE.
RP Hayakawa T., Nanno K., Kawai S., Katayama Y., Moriohshi N.;
RT "Molecular cloning and tissue-specific expression of two genes that encode caffeic acid O-methyltransferases from Populus kitchamiensis.", Plant Sci. 113:157-165 (1996).
RL FUNCTION: Catechols the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.
CC

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydrocinamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydrocinamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily family. COMT subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EM
CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this s
CC removed.
CC -----
DR EMBL; D49710; BAA08558.1; -, Genomic_DNA.
DR HSSP; P28002; 1K1Z.
DR SMR; Q43046; 5-364.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransferase.
DR InterPro; IPR001077; O_Mec_transf.
DR InterPro; IPR000051; SAM_bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF08100; Dimerisation; 1.
DR Pfam; PF00891; Methyltransferase_2; 1.
DR Lignin biosynthesis; Methyltransferase; Transferase.
SQ SEQUENCE 365 AA; 39791 MW; D6005B10FE55B83C CRC64;

Query Match 83.0%; Score 1588.5; DB 1; Length 3
Best Local Similarity 80.7%; Pred. No. 3.2e-117;
Matches 296; Conservative 36; Mismatches 32; Indels

QY 1 MGSSTETKMSPEBAABEAEAFVPMQLTSAVLPVMTKSAIEDVLEIM 15 60
DB 1 MGSSTETQMTPTQH--VSDEEAMLFAMQLASASVLPVMTKSAIELEIM 15 58

QY 61 TSDIASKLPTKQPDAAVMDRLRLASYSVLTCSRLTPDGKIRLRYGL 19 120
DB 59 TSEINSHLPTKQPDAAVMDRLRLASYSILTCSRLTPDGKIRLRYGL 19 118

QY 121 DDGVSIALSLNODKVLMSWYHLTEAVLEGIPFNKAYGMTAFEPHYGT 19 180
DB 119 EDGVSIVPLCLNODKVLMSWYHLKDVAIDGSIPTNKAYGMTAFEPHYGT 19 178

QY 181 GMSNSTITMKKILETTYKGFEGISVVDYGGGTGAHLNMIITAKYPMIKI 19 240
DB 179 GMSNSTITMKKILETTYKGFEGITSLVDYGGGTGAHVNTIVSKYPSIKI 19 238

QY 241 APSYGEVHGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP 19 300
DB 239 APSYGEVHGDMFVSVPNADAVFMKWI CHDMSDAHCLKFLKCCYDALP 19 298

QY 301 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGFEGFR 19 360
DB 299 ILVPAADSLPTKAVVHIDVIMLANPGKERTKEFEALAKAGAFQGRE 19 357

QY 361 IIEFLKK 367
DB 358 VIEFLKK 364

RESULT 8
COMTI_POPKI PRELIMINARY; PRT; 360 AA.
AC Q9M569;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Caffeic acid O-3-methyltransferase (Fragment).
OS Populus tomentosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots eustosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
NCBI_TaxId=118781;
TH 357

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jihanna W., Yentru S.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237777; AAF63200.1; -; mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q9M569; 5-360.
DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met. trans2.
DR InterPro; IPR000051; SAM bind.
DR InterPro; IPR011991; Wing hix DNA_bd.
DR Pfam; PF00891; Methyltransferase_2; 1.
DR Methyltransferase; transferase.
FT NON TER 360
SQ SEQUENCE 360 AA; 39174 MW; 40AC6D8EF1C1243D CRC64;

Query Match 82.5%; Score 1579.5; DB 2; Length 360;
Beet Local Similarity 81.0%; Pred. No. 1.6e-116;
Matches 294; Conservative 36; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSSTETKSPSEAAAEAEAFVFMQLTASAVLPVNLKSAIEDVLEIMAKAGAHIS 60
DB 1 MGSSTETQMTPTQ--VSDDEAHLFAMQLASASVLPMLIKTALELDLEIMAKAGCAFLIS 58
QY 61 TSDIASKLPKTPKPDAAVMDRLMLRLASYSVLTCSLRTIPDGKIERLYGLAYCQFLTN 120
DB 59 TSEIASHLPKTPKPDAPVMDRLRLRLASYSILTCSLKDPDKQVRELGLAPVCKEFLTN 118
QY 121 DDGVSIATSLMNODKVLMEISWYHLTEAVLEGGIPFNKAYGNTAFYHGTDPREFTVFN 180
DB 119 EGVGSVSPCLMNODKVLMEISWYHLKDALLEGGIPFNKAYGNTAFYHGTDRFNKVFNK 178
QY 181 GMSNSTITMKKILLETYKGFEGISVVDVGGGTGAHLMNIIAKYPMIKINFDLPHVID 240
DB 179 GMSDSTITMKKILLETYKGFEGITSLVDVGGGTGAVVNTIVSKYPSIKGINFDLPHVID 238
QY 241 APSYGEVEHVGDMFVSPKGDALFMKMI CHDWSDEHCKFLKCKYEALPTNGKTYLAE 300
DB 239 APSYGEVEHVGDMFVSPKADAVFMKMI CHDWSDAHCKFLKNCYDALPENGKTYLVLC 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHPGKERTKEFEALAKAGPEGFRVVAACAYNT 360
DB 299 ILPVAPDTSLATKGVVHIDVIMLAHPGKERTKEFEALAGAGQGFEMC-CAPNTH 357
QY 361 IIEFLK 363
DB 358 VIELRK 360

RESULT 9
O9LMB8_9ROSI PRELIMINARY; PRT; 364 AA.
AC O9LMB8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DS O-methyltransferase.
OS Populus trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosida I; Malpighiales; Salicaceae; Populus.
NCBI_Taxid=3695;
OX NCB1_Taxid=3695;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Dumas B., Van Doorselaere J., Legrand M., Van Montagu M.M., Inze D.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding

```

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CC alcohol that are incorporated into lignins (By similar:
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydro
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydro
CC cinnamate.
CC -I- PATHWAY: Lignin biosynthesis.
DR EMBL; M73431; AAF60951.1; -; mRNA.
DR HSSP; P28002; 1KYZ.
DR SMR; Q9LMB8; 5-363.
DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltran
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O Met. trans2.
DR InterPro; IPR000051; SAM bd.
DR InterPro; IPR011991; Wing_hix_DNA_bd.
DR Pfam; PF08100; Dimerisation; 1.
DR Pfam; PF00891; Methyltransferase_2; 1.
DR Lignin biosynthesis; Methyltransferase; Transferase.
SQ SEQUENCE 364 AA; 39724 MW; 033287E06443CD9C CRC64;

Query Match 82.4%; Score 1578.5; DB 2; Length 360;
Beet Local Similarity 80.6%; Pred. No. 2e-116;
Matches 295; Conservative 36; Mismatches 32; Indels 3;

QY 1 MGSSTETKSPSEAAAEAEAFVFMQLTASAVLPVNLKSAIEDVLEIM 60
DB 1 MGSSTETQMTPTQ--VSDDEAHLFAMQLASASVLPMLIKTALELDLEIM 58
QY 61 TSDIASKLPKTPKPDAAVMDRLMLRLASYSVLTCSLRTIPDGKIERLYGL 120
DB 59 TSEIASHLPKTPKPDAPVMDRLRLRLASYSILTCSLKDPDKQVRELGL 118
QY 121 DDGVSIATSLMNODKVLMEISWYHLTEAVLEGGIPFNKAYGNTAFYHGT 180
DB 119 EGVGSVSPCLMNODKVLMEISWYHLKDALLEGGIPFNKAYGNTAFYHGT 178
QY 181 GMSNSTITMKKILLETYKGFEGISVVDVGGGTGAHLMNIIAKYPMIKIN 240
DB 179 GMSDSTITMKKILLETYKGFEGITSLVDVGGGTGAVVNTIVSKYPSIKGI 238
QY 241 APSYGEVEHVGDMFVSPKGDALFMKMI CHDWSDEHCKFLKCKYEALP 300
DB 239 APSYGEVEHVGDMFVSPKADAVFMKMI CHDWSDAHCKFLKNCYDALP 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLAHPGKERTKEFEALAKAGPEGFR 360
DB 299 ILPVAPDTSLATKGVVHIDVIMLAHPGKERTKEFEALAGAGQGFEM 357
QY 361 IIEFLK 366
DB 358 VIELRK 363

RESULT 10
COMT1_MEDSA STANDARD; PRT; 365 AA.
ID COMT1_MEDSA
AC P28002;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl
DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC rosids; eustosida I; Fabales; Fabaceae; Papilionoideae; Trifl
OC Medicago.
OX NCB1_Taxid=3879;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Apollo;
RA Gowri G., Bugos R.C., Campbell W.H., Maxwell C.A., Dixon R.J.

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RT "Stress responses in alfalfa (*Medicago sativa* L.). X. Molecular cloning
 RT and expression of S-adenosyl-L-methionine:caffeic acid 3-O-
 methyltransferase, a key enzyme of lignin biosynthesis.";
 RL Plant Physiol. 97:7-14(1991).
 CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
 CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
 CC products that are subsequently be converted to the corresponding
 CC alcohols that are incorporated into lignins.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
 CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
 CC cinnamate.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- TISSUE SPECIFICITY: More abundant in roots and stems.
 CC -1- INDUCTION: By infection, plant wounding, or elicitor treatment of
 CC cell cultures.
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
 CC family. COMT subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: M63853; AAB46623.1; -, mRNA.
 DR PIR: T09673; T09673.
 DR PDB: 1KRW; X-ray; A/C/E=1-365.
 DR PDB: 1KYZ; X-ray; A/C/E=1-365.
 DR InterPro: IPR012967; Dimerisation.
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR001077; O Met trans2.
 DR InterPro: IPR000051; SAM_bd.
 DR InterPro: IPR011991; Wng_hlx_DNA_bd.
 DR Pfam: PF008100; Dimerisation; 1.
 DR Pfam: PF00891; Methyltransf_2; 1.
 KM 3D-structure; Lignin biosynthesis; Methyltransferase; Transferase.
 FT HELIX 16 27
 FT TURN 28 30
 FT HELIX 31 41
 FT TURN 42 43
 FT HELIX 44 49
 FT TURN 50 51
 FT TURN 53 54
 FT TURN 57 57
 FT STRAND 59 57
 FT HELIX 59 64
 FT TURN 65 65
 FT TURN 71 72
 FT HELIX 73 86
 FT TURN 87 88
 FT STRAND 90 96
 FT TURN 98 99
 FT STRAND 102 108
 FT HELIX 110 115
 FT TURN 119 120
 FT TURN 124 124
 FT TURN 125 131
 FT HELIX 132 132
 FT HELIX 134 137
 FT HELIX 138 142
 FT HELIX 143 149
 FT HELIX 153 158
 FT HELIX 162 165
 FT HELIX 166 168
 FT HELIX 170 194
 FT TURN 197 198
 FT STRAND 203 207
 FT TURN 208 210
 FT TURN 210 211
 FT HELIX 213 221
 FT TURN 223 224
 FT STRAND 226 231
 FT TURN 233 238
 FT TURN 243 244

FT STRAND 245 249
 FT TURN 252 254
 FT STRAND 262 263
 FT TURN 269 270
 FT HELIX 273 286
 FT STRAND 293 297
 FT STRAND 298 300
 FT STRAND 308 323
 FT HELIX 330 331
 FT STRAND 332 342
 FT HELIX 347 353
 FT STRAND 354 355
 FT TURN 356 361
 SQ SEQUENCE 365 AA; 39946 MW; C14B0D75F979C6B6 CRC64;
 Query Match 80.7%; Score 1544.5; DB 1; Length 3
 Best Local Similarity 78.8%; Pred. No. 9,7e-114;
 Matches 290; Conservative 42; Mismatches 33; Indels
 QY 1 MGSTETKMSPEEAAAEAFVPMQULTSASVLPMTLKSALDVLTK
 DB 1 MGSTGETQITPTH--ISDEKANLPAMQLASASVLPMTLKSALDLELTI
 QY 61 TSDIASKLPTKNPDAAVMLDRMLRLASYSVLTGSLRTLPDGKIRLYGL
 DB 59 PLEIASQLPTTNPDAPVMDRLRLACIYITGCVRTQDQDKVRLVGL
 QY 121 DDGVSIAALSINODKVLMSWYHLTEAVLEGGIPFNKAYGWTAFEVHGT
 DB 119 EDGVSISALNINQDKVLMESWYHLKDAVLVDGIGFNNAYGWTAFEVHGT
 QY 181 GMSNHSITTMKKILETYGFGFGLGSVDVGGTGALHLMIIAKYMIKI
 DB 179 GMSDSHITTMKKILETYGFGFGLKSLVDVGGTGAVINTIVSKYPTIKGI
 QY 241 APSYGVHVGSDMVSVPKGDAPFMKMICHDMSDEHCLFLKCYBALP
 DB 239 APSYGVHVGSDMVSIPKADAVPMKMICHDMSDEHCLFLKCYBALP
 QY 301 ILPVPDASLPKAVVHIDVIMLANPGKERTKTEKFEPAKAGAFEGFR
 DB 299 ILPVPDSSLATKGVVHIDVIMLANPGKERTQKEFPDLAKGAFQGRK
 QY 361 IIEFLKKI 368
 DB 358 IMEFLKKV 365
 RESULT 11
 COMTI_EUCGU STANDARD; PRT; 366 AA.
 AC P46484;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl
 DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOM
 GN Name=OMT;
 OS Bucalyptus Gunnii (Cider tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
 OC rosidae; Myrtales; Myrtaceae; Bucalyptus.
 OC NCBI_TaxID=3933;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=Xylem;
 RX MEDLINE=94345011; PubMed=8066135; DOI=10.1104/pp.105.2.749;
 RA Poeydomege O.; Boudet A.M.; Grima-Pettenati V.;
 RT "A cDNA encoding S-adenosyl-L-methionine:caffeic acid 3-O-
 RL methyltransferase from Bucalyptus.";
 CC Plant Physiol. 105:749-750(1994).
 CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
 CC and of 5-hydroxyferulic acid to sinapic acid. The resul


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CC products may subsequently be converted to the corresponding
CC alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC cinnamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC family. COMT subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: X74814, CAA52814.1; -, mRNA.
CC DR PIR: S40146, S40146.
CC DR HSSP: P28002, 1KYZ.
CC DR SMR: P46484, 7-364.
CC DR InterPro: IPR012967, Dimerisation.
CC DR InterPro: IPR001601, Methyltransf.
CC DR InterPro: IPR001077, O_Met_trans2.
CC DR InterPro: IPR000051, SAM_bd.
CC DR InterPro: IPR011991, Wing_hlx_DNA_bd.
CC DR Pfam: PF08100, Dimerisation; 1.
CC DR Pfam: PF00891, Methyltransf. 2; 1.
CC DR Lignin biosynthesis; Methyltransferase; Transferase.
CC DR KX SEQUENCE 366 AA; 39914 MW; 6B2385C3085AFABA CRC64;
SQ
Query Match 80.2%; Score 1535; DB 1; Length 366;
Best Local Similarity 78.2%; Pred. No. 5-113;
Matches 287; Conservative 45; Mismatches 31; Indels 4; Gaps 3;
QY 1 MGST-SETKMSSEAAAEBAFVPMQLTSSAVLPMVTKSAIEDVLEIMAKAGPGAH 59
DB 1 MGSTSEITQMTPTQ--VSDBEANLPMQQLASASVLPMTVKAIEIDLRLIMAKAGPGAF 58
QY 60 STSDIASKLPPTNPDAAVWLDMLRLASVYLTGSLRTLPQGIKRLGLA-PVCKFLFR 119
DB 59 SGGEVAQAQPTQNPPEAPVMDRIFFLLASYSVITCTRLNLPQKVERLGLAPVCKFLVK 118
QY 120 NDDGVSAIALSLMNDQKVLMSWYHLTEAVLBGGIIPFNKAYGWTAEYHGTDPREVTVEN 179
DB 119 NDDGVSAIALSLMNDQKVLMSWYVYKDAVLEGGIIPFNKAYGWTAEYHGTDPREFKIEN 178
QY 180 NGSMSHSTITMKKILETYGFGELGSVVDVGGTGAMLMITAKTPMITGTFPDLPHVIE 239
DB 179 RSMDSHSTITMKKILETYGFGELGVVDVGGTGAVLSMIVAKYPSMKGINFDPHIVIE 238
QY 240 EAPSYPGVHVGQDMVSVPKGDAIPMKWICHDMSEHCLKFLKCKCYEALPTNGKVIILAE 299
DB 239 DAPPLBGVHVGQDMVSVPKGDAIPMKWICHDMSDHCKAKFLKCYDLPNIGKVIILAE 298
QY 300 CILPVAPDASLPKAVHVIDVIMLANPGKERTKEFEALAKGAGFEGFRVASCAYNT 359
DB 299 CILPVVPDTSLATKQVITHDCIMLANPGKERTQKEFETLAKGAGFGQFQWVC-CAFGT 357
QY 360 WIEEFLK 366
DB 358 HYMEFLK 364
RESULT 12
COMT1 CLABR STANDARD; PRT; 370 AA.
AC 023760;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-
GN methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT) .
Name=COMT;
Q5 Clarkia breweri.
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CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
CC rosidae; Myrtales; Onagraceae; Clarkia.
CC NCBI_TaxID=36903;
CC [1]
CC RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 3-13.
CC RA Wang J., Pichersky E.;
CC RT "Nucleotide sequence of S-adenosyl-L-methionine:caffeic aci
CC methyltransferase from Clarkia breweri."
CC RT (er) Plant Gene Register PCR97-104.
CC [2]
CC RN MUTAGENESIS OF 132-LEU-CYS-133; 135-MET--GLN-137 AND 166-THI
CC RP MEDLINE=99345902; PubMed=10415125; DOI=10.1006/abdi.1999.131
CC RA Wang J., Pichersky E.;
CC RT "Identification of specific residues involved in substrate
CC discrimination in two plant O-methyltransferases."
CC RL Arch. Biochem. Biophys. 368:172-180(1999).
CC CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
CC and of 5-hydroxyferulic acid to sinapic acid. The resulti
CC products may subsequently be converted to the correspon
CC alcohols that are incorporated into lignine.
CC CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihyd
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hyd
CC cinnamate.
CC CC -1- PATHWAY: Lignin biosynthesis.
CC CC -1- SUBUNIT: Homodimer.
CC CC -1- MISCELLANEOUS: Caffeic acid 3-O-methyltransferase (COMT
CC has distinct substrate specificity from (iso)eugenol O-
CC methyltransferases (IEMT), a highly homologous enzyme, t
CC methylates the hydroxyl group at the meta position rath
CC the para position as IEMT does.
CC CC -1- SIMILARITY: Belongs to the methyltransferase superfamily;
CC family. COMT subfamily.
CC -----
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CC the European Bioinformatics Institute. There are no restri
CC use as long as its content is in no way modified and this st
CC removed.
CC -----
CC EMBL: AF006009; AAB71141.1; -, mRNA.
CC DR HSSP: P28002, 1KYZ.
CC DR SMR: O23760, 7-368.
CC DR InterPro: IPR012967, Dimerisation.
CC DR InterPro: IPR001601, Methyltransf.
CC DR InterPro: IPR001077, O_Met_trans2.
CC DR InterPro: IPR000051, SAM_bd.
CC DR InterPro: IPR011991, Wing_hlx_DNA_bd.
CC DR Pfam: PF08100, Dimerisation; 1.
CC DR Pfam: PF00891, Methyltransf. 2; 1.
CC DR Direct protein sequencing; Lignin biosynthesis; Methyltransf
CC Transferase.
CC KM MUTAGEN 132 133
CC FT IC->FL: Decreases substrate
CC FT discrimination. Substrate pref
CC FT changed; when associated with
CC FT or 135-TAT-137 and 166-NE-167.
CC FT KMNO->TAT: Decreases substrate
CC FT discrimination. Substrate pref
CC FT changed; when associated with
CC FT or 166-NE-167 or 132-PL-133 and
CC FT 167.
CC FT TA->NE: No effect on substrate
CC FT preference; substrate preferen
CC FT when associated with 135-TAT-1;
CC FT FL-133 and 135-TAT-137.
CC SQ SEQUENCE 370 AA; 40262 MW; 8ADC2F626FCB87CA CRC64;
Query Match 79.8%; Score 1528; DB 1; Length 370
Best Local Similarity 78.2%; Pred. No. 2e-112;
Matches 290; Conservative 42; Mismatches 31; Indels
QY 1 MGST--SETKMSSEAAAEBAFVPMQLTSSAVLPMVTKSAIEDVLEIMAKAGPGAH 59
DB 1 MGSTSEITQMTPTQ--VSDBEANLPMQQLASASVLPMTVKAIEIDLRLIMAKAGPGAF 58
QY 60 STSDIASKLPPTNPDAAVWLDMLRLASVYLTGSLRTLPQGIKRLGLA-PVCKFLFR 119
DB 59 SGGEVAQAQPTQNPPEAPVMDRIFFLLASYSVITCTRLNLPQKVERLGLAPVCKFLVK 118
QY 120 NDDGVSAIALSLMNDQKVLMSWYHLTEAVLBGGIIPFNKAYGWTAEYHGTDPREVTVEN 179
DB 119 NDDGVSAIALSLMNDQKVLMSWYVYKDAVLEGGIIPFNKAYGWTAEYHGTDPREFKIEN 178
QY 180 NGSMSHSTITMKKILETYGFGELGSVVDVGGTGAMLMITAKTPMITGTFPDLPHVIE 239
DB 179 RSMDSHSTITMKKILETYGFGELGVVDVGGTGAVLSMIVAKYPSMKGINFDPHIVIE 238
QY 240 EAPSYPGVHVGQDMVSVPKGDAIPMKWICHDMSEHCLKFLKCKCYEALPTNGKVIILAE 299
DB 239 DAPPLBGVHVGQDMVSVPKGDAIPMKWICHDMSDHCKAKFLKCYDLPNIGKVIILAE 298
QY 300 CILPVAPDASLPKAVHVIDVIMLANPGKERTKEFEALAKGAGFEGFRVASCAYNT 359
DB 299 CILPVVPDTSLATKQVITHDCIMLANPGKERTQKEFETLAKGAGFGQFQWVC-CAFGT 357
QY 360 WIEEFLK 366
DB 358 HYMEFLK 364
MUTAGEN 166 167
FT TA->NE: No effect on substrate
FT preference; substrate preferen
FT when associated with 135-TAT-1;
FT FL-133 and 135-TAT-137.
SQ SEQUENCE 370 AA; 40262 MW; 8ADC2F626FCB87CA CRC64;
Query Match 79.8%; Score 1528; DB 1; Length 370
Best Local Similarity 78.2%; Pred. No. 2e-112;
Matches 290; Conservative 42; Mismatches 31; Indels
QY 1 MGST--SETKMSSEAAAEBAFVPMQLTSSAVLPMVTKSAIEDVLEIMAKAGPGAH 59
DB 1 MGSTSEITQMTPTQ--VSDBEANLPMQQLASASVLPMTVKAIEIDLRLIMAKAGPGAF 58
QY 60 STSDIASKLPPTNPDAAVWLDMLRLASVYLTGSLRTLPQGIKRLGLA-PVCKFLFR 119
DB 59 SGGEVAQAQPTQNPPEAPVMDRIFFLLASYSVITCTRLNLPQKVERLGLAPVCKFLVK 118
QY 120 NDDGVSAIALSLMNDQKVLMSWYHLTEAVLBGGIIPFNKAYGWTAEYHGTDPREVTVEN 179
DB 119 NDDGVSAIALSLMNDQKVLMSWYVYKDAVLEGGIIPFNKAYGWTAEYHGTDPREFKIEN 178
QY 180 NGSMSHSTITMKKILETYGFGELGSVVDVGGTGAMLMITAKTPMITGTFPDLPHVIE 239
DB 179 RSMDSHSTITMKKILETYGFGELGVVDVGGTGAVLSMIVAKYPSMKGINFDPHIVIE 238
QY 240 EAPSYPGVHVGQDMVSVPKGDAIPMKWICHDMSEHCLKFLKCKCYEALPTNGKVIILAE 299
DB 239 DAPPLBGVHVGQDMVSVPKGDAIPMKWICHDMSDHCKAKFLKCYDLPNIGKVIILAE 298
QY 300 CILPVAPDASLPKAVHVIDVIMLANPGKERTKEFEALAKGAGFEGFRVASCAYNT 359
DB 299 CILPVVPDTSLATKQVITHDCIMLANPGKERTQKEFETLAKGAGFGQFQWVC-CAFGT 357
QY 360 WIEEFLK 366
DB 358 HYMEFLK 364
MUTAGEN 166 167
FT TA->NE: No effect on substrate
FT preference; substrate preferen
FT when associated with 135-TAT-1;
FT FL-133 and 135-TAT-137.
SQ SEQUENCE 370 AA; 40262 MW; 8ADC2F626FCB87CA CRC64;
```

DB 1 MGSQTGAETQTLPTHT--VSDEANLPMQQLASASVLPVWLKKAILEDLVLEIMAKSIPIHGS 58
QY 56 GAHITSIDIASLPTKPNPDAAVMDRLMLLASVYLTCSTLTTPDGKIERLYGALPCK 115
DB 59 GAYISPAEIAQQLPTTNPDAFVMDLRVLRLTLASYSVWTCISLELDGKIERLYGALPCK 118
QY 116 FLTRDDGVSTIAALSIMNODKYLMSWYHLTEAVLEGIPFNKAYGMTAFEHGHTDPPFN 175
DB 119 FLTKNEDEVSLAPLCLMMDKYLMSWYHLKDALIDGGIPFNKAYGMTAFEHGHTDPPFN 178
QY 176 TVFNNGMSNSTIITMKILLETYGFEGSLGVVDVGGTGGAHLNMIITAKYPMIKGINPDL 235
DB 179 KYFNKMGSDHSITITMKILFEMVTGFELANTITVDVGGTGGAVALSMIVAKKPSIKGINPDL 238
QY 236 HVIEEAPSYGVEHVGDMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYALPTNGKV 295
DB 239 HVIEDAPITPGVEHVGDMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYALTEHGV 298
QY 296 ILAECILVAPDASLPTKAVVHIDVIMLANPGKERTKEPEALAKGAFEPFVNASC 355
DB 299 IVAECILVSPSPSLATKGVHIDVIMLANPGKERTKEPEALAKGAFEPFVNASC 357
QY 356 AYNTHWIEFLK 366
DB 358 AFTYVMEFLK 368

RESULT 13
COMT1 CAPAN STANDARD; PRT; 359 AA.
AC 09RGYB; P93088;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
GN Name=COMT;
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxId=4072;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=pericarp;
RA Lee B.-H., Choi D., Lee K.-W.;
RA "Isolation and characterization of o-diphenol-O-methyltransferase cDNA
RT clone in hot pepper (Capsicum annuum L.).";
RL J. Plant Biol. 41:9-14(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Chungyang; TISSUE=Root;
RA Kim K.-W., Lee S.-W.;
RA "Isolation and characterization of caffeic acid O-methyltransferase
RT cDNA from Capsicum annuum.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC products may subsequently be converted to the corresponding
CC alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC cinnamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- TISSUE SPECIFICITY: Fruit. Not expressed in leaf.
CC -1- DEVELOPMENTAL STAGE: Expression increases during fruit development
CC but decreases during ripening.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC family. COMT subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this s
CC removed.
CC EMBL; U83789; AAC1745.1; -; mRNA.
CC EMBL; AF212316; AAG43822.1; -; mRNA.
CC HSSP; P28002; 1KYZ.
DR SMR; Q9FOX8; 11-359.
DR InterPro; IPR012967; Dimerisation.
DR InterPro; IPR001601; Methyltransfer.
DR InterPro; IPR001077; O_Met_transf.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00891; Methyltransferase_1.
DR Pfam; PF08100; Dimerisation; 1.
KM Lignin biosynthesis; Methyltransferase; Transferase.
FT CONFLICT 71 V -> I (in Ref. 2).
FT CONFLICT 246 R -> G (in Ref. 2).
SQ SEQUENCE 359 AA; 39433 MW; 70599AED75CE1730 CRC64;
Query Match 79.8%; Score 1527.5; DB 1; Length 3
Best Local Similarity 77.9%; Pred. No. 2.1e-112;
Matches 285; Conservative 35; Mismatches 39; Indels

QY 1 MGSSTETKMSPEAAAEBAFVPMQLTSSASVLPVWLKKAILEDLVLEIM 1S 60
DB 1 MDSTNQ-----NLQTDEAFLPMQLASASVLPVWLKKAILEDLVLEIM 1S 54
QY 61 TSDIAŠKLPTKNPDAAVMDRLMLLASVYLTCSTLTTPDGKIERLYG 1N 120
DB 55 PSEILAQPLTKNPEAPVMDRLMLLASVYLTCSTLTTPDGKIERLYG 1N 114
QY 121 DDGVSTIALSLMNODKYLMSWYHLTEAVLEGIPFNKAYGMTAFEVGT 1N 180
DB 115 ADGVSAVPLLMNODKYLMSWYHLTDVLDGVGFENAYGMTAFEVGT 1N 174
QY 181 GMSNSTITTMKKILETYGFEGSLGVVDVGGTGGAHLNMIITAKYPMIKGI 1E 240
DB 175 GMSDHSITMTKKILEDYGFEGSLGVVDVGGTGGAHLNMIITAKYPMIKGI 1E 234
QY 241 APSYGVHVGDMFVSVPKGDALFMKMICHDMSDEHCLKFLKCYEALP 1E 300
DB 235 APAYGVHVGDMFVSVPKADALFMKMICHDMSDEHCLKFLKCYEALP 1E 294
QY 301 ILVAPDASLPTKAVVHIDVIMLANPGKERTKEPEALAKGAFEPFGR 1T 360
DB 295 ILPEPDTLSAATKAVHIDVIMLANPGKERTKEPEALAKGAFEPFGR 1T 353
QY 361 IIEFLK 366
DB 354 VMEFLK 359

RESULT 14
COMT1 OCIBA STANDARD; PRT; 361 AA.
AC 09XGW0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (Name=COMT1);
GN Ocimum basilicum (Sweet basil).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Lamiales; Lamiales; Nepetoideae; Ocimeae
OX NCBI_TaxId=39350;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. EMK-1;
RA Wang J., Dudareva N., Kish C.M., Simon J.E., Lewinson E., Pichersky E.;
RA "Nucleotide sequences of two cDNAs encoding caffeic acid O-

RT methyltransferases from sweet basil (Ocimum basilicum).";
RU (er) Plant Gene Register PCR99-105
CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC products may subsequently be converted to the corresponding
CC alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC cinnamate
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Type 2
CC family. COMT subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF154917; AAD38189.1; -; mRNA.
CC DR HSSP: P28002; 1KYZ.
CC DR SMR: Q9XGW0; 3-361.
CC DR InterPro: IPR012967; Dimerisation.
CC DR InterPro: IPR001601; Methyltransf.
CC DR InterPro: IPR001077; O-Met. trans2.
CC DR InterPro: IPR000051; SAM bd.
CC DR InterPro: IPR011991; Wing_hlx_DNA_bd.
CC DR Pfam: PF08100; Dimerisation; 1.
CC DR Pfam: PF00891; Methyltransf_2; 1.
CC DR Lignin biosynthesis; Methyltransferase; Transferrase.
CC KW Lignin biosynthesis; Methyltransferase; Transferrase.
CC SQ SEQUENCE 361 AA; 39529 MW; D6ABC3DC837AC9E CRC64;

Query Match 79.6%; Score 1523.5; DB 1; Length 361;

Best Local Similarity 78.1%; Pred. No. 4.4e-112; Matches 286; Conservative 35; Mismatches 40; Indels 5; Gaps 2;

QY 1 MGSTSETKMSPEEAAAEEBAFVPMQVLSASVLPVWLKSAIELDVLEITMAAGGAAHS 60
DB 1 MGSANTPTQIND-----EEENLFPMQLASASVLPVWLKSAIELDLEIKSGAGAFVS 56
QY 61 TSDIASKLPYKNPDAVWLDRLRLASYSVLTGSLRTLPDGKIRLYGLAFVCKELTEN 120
DB 57 PVDLAQAQPTTPDAVWLDRLRLASYSVLTGSLRTLPDGKIRLYGLAFVCKELTEN 116
QY 121 DDGVSIALSLNDKYLWESVYHLTEAVLEGIPNNKAYGNTAFRYGTDPRFTVFN 180
DB 117 EDGVSMAPLTLMNQDKVLMESVYHLSDAVVDGIPNNKAYGNTAFRYGTDPRFKVFNQ 176
QY 181 GMSNSTITMKKILETYKGFEGLSVVDVGSGTAHLNMIIAKYPMIKGINFDLPHVIEE 240
DB 177 GMSNSTITMKKILETYKGFEGLSVVDVGSGTAHLNMIIVSKTISIKGINFDLPHVIED 236
QY 241 APSYGVHEVGDMPVSVPKGDAIFMKWICHMWSDEHCLKFKCYEALPTNGKYLAE 300
DB 237 APSYGVHEVGDMPVSVPKGDAIFMKWICHMWSDEHCLKFKCYEALPTNGKYLAE 296
QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGREGRRVVASCAVNTW 360
DB 297 VLPVPADGLATKAVVHIDVIMLAHNPCKERTKEFEALAGAGREGRRVVASCAVNTW 355
QY 361 IIEFLK 366
DB 356 IMELLK 361

RESULT 15
COMT3 POPKI STANDARD; PRT; 364 AA.
AC Q43047;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Caffeic acid 3-O-methyltransferase 3 (EC 2.1.1.68) (S-adenosyl-L-

DE methionine:caffeic acid 3-O-methyltransferase 1) (COMT-3) ((
CN Name=COMT3;
OS Populus kitakamiensis (Aspen).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC rosids; eucosids I; Malpighiales; Salicaceae; Salicaceae; Pop
OX NCBI_Taxid=3698;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hayakawa T., Nanto K., Kawai S., Katayama Y., Morohoshi N.;
RT "Molecular cloning and tissue-specific expression of two gen
RT encode caffeic acid O-methyltransferases from Populus kitak
RU Plant Sci. 113:157-165(1996).
CC -1- FUNCTION: Catalyzes the conversion of caffeic acid to f
CC and of 5-hydroxyferulic acid to sinapic acid. The result
CC products may subsequently be converted to the correspon
CC alcohols that are incorporated into lignins.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihyd
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hyd
CC cinnamate.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily;
CC family. COMT subfamily.
CC -----
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CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this st
CC removed.
CC -----
CC EMBL: D49711; BAA08559.1; -; Genomic DNA.
CC DR HSSP: P28002; 1KYZ.
CC DR SMR: Q43047; 5-363.
CC DR InterPro: IPR012967; Dimerisation.
CC DR InterPro: IPR001601; Methyltransf.
CC DR InterPro: IPR001077; O-Met. trans2.
CC DR InterPro: IPR000051; SAM bd.
CC DR InterPro: IPR011991; Wing_hlx_DNA_bd.
CC DR Pfam: PF00891; Methyltransf_2; 1.
CC DR Pfam: PF08100; Dimerisation; 1.
CC DR Lignin biosynthesis; Methyltransferase; Transferrase.
CC KW Lignin biosynthesis; Methyltransferase; Transferrase.
CC SQ SEQUENCE 364 AA; 39576 MW; 6322956A988E6C1 CRC64;

Query Match 78.9%; Score 1511; DB 1; Length 364
Best Local Similarity 77.7%; Pred. No. 4.3e-111; Matches 285; Conservative 39; Mismatches 39; Indels 3;

QY 1 MGSTSETKMSPEEAAAEEBAFVPMQVLSASVLPVWLKSAIELDVLEITW 60
DB 1 MGSITGETMSP--AQIDDEEA-NFAMQLISSSVLPVWLKTAIELDLEITW 57
QY 61 TSDIASKLPYKNPDAVWLDRLRLASYSVLTGSLRTLPDGKIRLYGL 120
DB 58 PSDIASHLPTKNPDAVWLDRLRLASYSVLTGSLRTLPDGKIRLYGL 117
QY 121 DDGVSIALSLNDKYLWESVYHLTEAVLEGIPNNKAYGNTAFRYGNT 180
DB 118 EDGVSVSPCLMNDKYLWESVYHLKQALIEGGIPNNKAYGNTAFRYGNT 177
QY 181 GMSNSTITMKKILETYKGFEGLSVVDVGSGTAHLNMIIAKYPMIKGIN 240
DB 178 GMSDHSKMAKKILIESYKGFEGLSVVDVGSGTAHVSTIVSKTSPSII 237
QY 241 APSYGVHEVGDMPVSVPKGDAIFMKWICHMWSDEHCLKFKCYEALP 300
DB 238 APAFPGVENVGDMFVSVPKADAVFMKWIICHMWSDEHCLRLKNCYDALP 297
QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKEFEALAGAGREGRR 360
DB 298 ILPVPADTSLATKAVVHIDVIMLAHNPCKERTKEFEALAGAGREGRR 356
QY 361 IIEFLK 367

Mon Dec 12 10:52:55 2005

us-10-681-878a-6.rup

ge 11

Db 357 VIEFRKQ 363

Search completed: December 12, 2005, 08:37:26
Job time : 234 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 08:30:15, Search time 46 Seconds
(without alignments)
661.405 Million cell updates/sec

Title: US-10-681-878a-6
Perfect score: 1915
Sequence: 1 MGS1ETKMSPEAAAE...FRVASCANWTITFLKKI 368

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RG_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1915	100.0	368	2	US-08-991-677-6 Sequence 6, Appl
2	1595.5	83.3	365	1	US-08-715-325-2 Sequence 2, Appl
3	1595.5	83.3	365	2	US-09-947-027-6 Sequence 6, Appl
4	1572.5	82.1	364	1	US-08-204-288-2 Sequence 2, Appl
5	1566.5	81.8	365	2	US-09-500-569-4 Sequence 4, Appl
6	1566.5	81.8	365	2	US-09-971-823B-4 Sequence 4, Appl
7	1499.5	78.3	364	1	US-08-204-288-5 Sequence 5, Appl
8	1492	77.9	358	2	US-09-500-569-18 Sequence 18, Appl
9	1492	77.9	358	2	US-09-971-823B-18 Sequence 18, Appl
10	1244	65.0	356	2	US-09-500-569-6 Sequence 6, Appl
11	1244	65.0	356	2	US-09-971-823B-6 Sequence 6, Appl
12	1073	56.0	362	2	US-09-500-569-14 Sequence 14, Appl
13	1073	56.0	362	2	US-09-971-823B-14 Sequence 14, Appl
14	1047	54.7	365	1	US-08-186-833-4 Sequence 7, Appl
15	1045.5	54.6	365	1	US-08-204-288-7 Sequence 12, Appl
16	988.5	51.6	354	2	US-09-500-569-12 Sequence 12, Appl
17	988.5	51.6	354	2	US-09-971-823B-12 Sequence 12, Appl
18	964.5	50.4	264	2	US-09-598-401C-78 Sequence 78, Appl
19	947	49.5	305	2	US-09-500-569-2 Sequence 2, Appl
20	947	49.5	305	2	US-09-971-823B-2 Sequence 2, Appl
21	779.5	40.7	231	2	US-09-500-569-20 Sequence 20, Appl
22	779.5	40.7	231	2	US-09-971-823B-20 Sequence 20, Appl
23	771	40.3	378	2	US-09-500-569-10 Sequence 10, Appl
24	771	40.3	378	2	US-09-971-823B-10 Sequence 10, Appl
25	726	37.9	371	2	US-09-500-569-16 Sequence 16, Appl
26	726	37.9	371	2	US-09-971-823B-16 Sequence 16, Appl
27	667	34.8	328	2	US-09-615-192A-274 Sequence 274, App

28	500.5	26.1	174	2	US-09-500-569-26 Sequ	Appl
29	500.5	26.1	174	2	US-09-971-823B-26 Sequ	Appl
30	479	25.0	198	2	US-09-615-192A-771 Sequ	App
31	413.5	21.6	156	2	US-09-615-192A-272 Sequ	App
32	376.5	19.7	160	2	US-09-615-192A-275 Sequ	App
33	372	19.4	188	2	US-09-500-569-8 Sequ	Appl
34	372	19.4	188	2	US-09-971-823B-8 Sequ	Appl
35	365	19.1	145	2	US-09-615-192A-270 Sequ	App
36	356.5	18.6	94	1	US-08-266-451B-20 Sequ	Appl
37	356.5	18.6	94	1	US-08-748-725-20 Sequ	Appl
38	291.5	15.2	313	2	US-09-902-540-9934 Sequ	App
39	272.5	14.2	363	1	US-08-845-742-2 Sequ	Appl
40	259	13.5	362	2	US-09-758-759-196 Sequ	App
41	254.5	13.3	332	2	US-09-724-797-18 Sequ	Appl
42	249.5	13.0	351	2	US-09-266-965-133 Sequ	App
43	226	11.8	82	2	US-09-500-569-24 Sequ	Appl
44	226	11.8	82	2	US-09-971-823B-24 Sequ	Appl
45	217.5	11.4	345	2	US-09-059-522-5 Sequ	Appl
46	217.5	11.4	345	2	US-09-382-027-5 Sequ	Appl
47	212.5	11.1	621	2	US-09-059-522-1 Sequ	Appl
48	212.5	11.1	621	2	US-09-382-027-1 Sequ	Appl
49	211.5	11.0	452	2	US-09-059-522-3 Sequ	Appl
50	211.5	11.0	452	2	US-09-382-027-3 Sequ	Appl
51	186.5	9.7	356	1	US-07-959-941-2 Sequ	Appl
52	186.5	9.7	356	1	US-08-259-924-2 Sequ	Appl
53	173	9.0	115	2	US-09-266-965-4 Sequ	Appl
54	171.5	9.0	123	2	US-09-500-569-28 Sequ	Appl
55	171.5	9.0	123	2	US-09-971-823B-28 Sequ	Appl
56	166.5	8.7	109	2	US-09-500-569-22 Sequ	Appl
57	166.5	8.7	109	2	US-09-971-823B-22 Sequ	Appl
58	147.5	7.7	117	2	US-09-266-965-5 Sequ	Appl
59	146	7.6	115	2	US-09-266-965-3 Sequ	Appl
60	141	7.4	125	2	US-09-902-540-10705 Sequ	App
61	112.5	5.9	368	2	US-09-252-991A-20452 Sequ	App
62	107	5.6	139	2	US-09-252-991A-20476 Sequ	App
63	100.5	5.2	308	1	US-08-457-245-8 Sequ	Appl
64	91.5	4.8	237	1	US-08-576-626A-58 Sequ	App
65	91	4.8	379	2	US-09-489-039A-12857 Sequ	App
66	89.5	4.7	573	2	US-09-134-000C-5258 Sequ	App
67	89.5	4.7	482	2	US-09-252-991A-17621 Sequ	App
68	89	4.6	908	2	US-09-489-039A-14097 Sequ	App
69	89	4.6	908	2	US-09-949-016-6961 Sequ	App
70	88.5	4.6	522	2	US-09-902-540-12872 Sequ	App
71	86.5	4.5	437	2	US-09-602-777A-84 Sequ	App
72	86	4.5	439	2	US-09-134-000C-6557 Sequ	App
73	86	4.5	483	2	US-08-378-313-31 Sequ	App
74	85.5	4.5	603	2	US-08-687-865A-2 Sequ	Appl
75	85.5	4.5	603	2	US-09-043-711-2 Sequ	Appl
76	85.5	4.5	3170	2	US-07-642-734C-5 Sequ	Appl
77	85.5	4.5	3170	2	US-08-439-009A-5 Sequ	Appl
78	84.5	4.4	911	1	US-08-596-985-2 Sequ	Appl
79	84	4.4	268	2	US-09-543-681A-7944 Sequ	App
80	84	4.4	290	2	US-09-543-681A-4737 Sequ	App
81	84	4.4	614	2	US-10-104-047-3276 Sequ	App
82	84	4.4	897	2	US-09-543-681A-4249 Sequ	App
83	83	4.3	510	2	US-08-801-344-8 Sequ	Appl
84	83	4.3	510	2	US-09-498-599-8 Sequ	Appl
85	82.5	4.3	527	2	US-09-248-796A-16016 Sequ	App
86	82.5	4.3	1315	2	US-08-913-880C-1 Sequ	Appl
87	82	4.3	485	2	US-08-378-313-30 Sequ	Appl
88	82	4.3	803	2	US-08-062-368-4 Sequ	Appl
89	81.5	4.3	609	2	US-09-115-475-19 Sequ	Appl
90	81.5	4.3	609	2	US-09-115-475-22 Sequ	Appl
91	81.5	4.3	671	1	US-08-737-716-13 Sequ	Appl
92	81.5	4.3	769	2	US-09-543-681A-7175 Sequ	App
93	81.5	4.3	3144	1	US-08-246-982A-6 Sequ	Appl
94	81.5	4.3	3144	1	US-08-453-255-6 Sequ	Appl
95	81.5	4.3	3144	1	US-08-457-273B-42 Sequ	Appl
96	81.5	4.3	3144	2	US-08-556-419-21 Sequ	Appl
97	81.5	4.3	3144	2	US-09-041-886-15 Sequ	Appl
98	81.5	4.3	3144	2	US-09-538-092-1118 Sequ	App
99	81	4.2	245	2	US-09-724-797-14 Sequ	App
100	81	4.2	313	2	US-09-134-001C-3628 Sequ	App

ALIGNMENTS

RESULT 1
US-08-991-677-6
Sequence 6, Application US/08991677A
Patent No. 6252135
GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carriaway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 368
TYPE: PR1
ORGANISM: Liguidambar styraciflua
US-08-991-677-6

Query Match 100.0%; Score 1915; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.9e-204;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSTSETKMSPSBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEIMAKAGPAHIS	60
DB	1	MGSTSETKMSPSBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEIMAKAGPAHIS	60
QY	61	TSDIASKLPTKNPDAVWMLDRMLRLASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTEN	120
DB	61	TSDIASKLPTKNPDAVWMLDRMLRLASYSVLTCSLRTLPDGKIERLYGLAPVCKFLTEN	120
QY	121	DDGVSTAAISLNMQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDRPNTVFN	180
DB	121	DDGVSTAAISLNMQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGTDRPNTVFN	180
QY	181	GMSNHSITTMKKILETYGFGFGLSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE	240
DB	181	GMSNHSITTMKKILETYGFGFGLSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPVIEE	240
QY	241	APSYGVEHVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKVI LAEC	300
DB	241	APSYGVEHVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALPTNGKVI LAEC	300
QY	301	ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAKGAGFEGRRVASCAYNTW	360
DB	301	ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAKGAGFEGRRVASCAYNTW	360
QY	361	IIIEFLKKI 368	
DB	361	IIIEFLKKI 368	

RESULT 2
US-08-715-325-2
Sequence 2, Application US/08715325
Patent No. 5886243
GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Teal, Chung-Tui
APPLICANT: Podila, Gopi
TITLE OF INVENTION: Genetic Engineering of Wood Color
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Michael, Best & Friedrich

STREET: 100 E. Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: United States of America
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: WordPerfect for Windows 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,325
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/007727
FILING DATE: 30 NOV 1995
ATTORNEY/AGENT INFORMATION:
NAME: Gemignani, Joseph A
REGISTRATION NUMBER: 19,482
REFERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-6560
TELEFAX: (414) 277-0656
TELEX: 262057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: no
US-08-715-325-2

Query Match 83.3%; Score 1595.5; DB 1; Length 365;
Best Local Similarity 80.9%; Pred. No. 7.8e-169;
Matches 297; Conservative 37; Mismatches 30; Indels 2;

QY	1	MGSTSETKMSPSBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEIM	60
DB	1	MGSTSETKMSPSBAABEAEAFVPMQLTSASVLPVMTLSAIELDVLEIM	60
QY	61	TSDIASKLPTKNPDAVWMLDRMLRLASYSVLTCSLRTLPDGKIERLYGL	120
DB	59	TSEIASHLPTKNPDAVWMLDRMLRLASYSVLTCSLRTLPDGKIERLYGL	118
QY	121	DDGVSTAAISLNMQDKVLMESWYHLTEAVLEGGIPFNKAYGWTAFYHGT	180
DB	119	EDGVSVSPCLCMNQDKVLMESWYHLKDAILDGGIPFNKAYGWTAFYHGT	178
QY	181	GMSNHSITTMKKILETYGFGFGLSVVDVGGGTGAHLNMIIAKYPMIGII	240
DB	179	GMSDHSITTMKKILETYGFGFGLSLVDVGGGTGAHVNTIVSKYPSIGII	238
QY	241	APSYGVEHVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP	300
DB	239	APSYGVEHVGGDMFVSPKGDALFMKWI CHDMSDEHCLKFLKCCYEALP	298
QY	301	ILPVPADASLPTKAVVHIDVIMLAHNPCKERTKTEKFEALAKGAGFEGRR	360
DB	299	ILPVPADTSLATKGVVHIDVIMLAHNPCKERTKTEKFEALAKGAGFQFEE	357
QY	361	IIIEFLKK 367	
DB	358	VIEFRKK 364	

RESULT 3
US-09-947-027-6
Sequence 6, Application US/09947027
Patent No. 685864
GENERAL INFORMATION:

APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Lajeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIO
FILE REFERENCE: 066040-9718
CURRENT APPLICATION NUMBER: US/09/947,027
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in version 3.0
SEQ ID NO: 6
LENGTH: 365
TYPE: prt
ORGANISM: aspen populus tremuloides
US-09-947-027-6

Query Match 83.3%; Score 1595.5; DB 2; Length 365;
Best Local Similarity 80.9%; Pred. No. 7.8e-169;
Matches 297; Conservative 37; Mismatches 30; Indels 3; Gaps 2;

QY 1 MGSTETKMSPEAAAEAEAFVPMOLTSASVLPVMTKSAIELDVLEIMAKAGCAHIS 60
1 MGSTETQMTPTQ--VSDEAHLPANQLASASVLPMLTKTALIEDLLEIMAKAGCAHIS 58
DB 61 TSDIASKLPTRKPDPAVMDRLRLASYSVLTCSLRTLPDGIKIERLYGLAVYCKFLTRN 120
59 TSEIASHLPTRKPDPAVMDRLRLRLASYSILTCSLKDLPDGIKIERLYGLAVYCKFLTRN 118
QY 121 DDGVSIALSLMNOCKVLMESWYHLTEAVLLEGIPFNKAYGWTAFEGHTDPRFNTVFN 180
119 EDGVSVPCLMNOCKVLMESWYHLKDAILDGIIPFNKAYGWTAFEGHTDPRFNTVFN 178
DB 181 GMSNSTITMKKILETYKGFEGISVVDVGSGTGALNMIIAKYPMIKGINFDLPHVIEE 240
179 GMSDSTITMKKILETYKGFEGISVVDVGSGTGAVVNTIVSKYPSIKGINFDLPHVIED 238
QY 241 APSYGEVHVGDMFVSVPKGDALFMKNI CHDMSDEHCLKFLKCYEALPTNGKYLAE 300
239 APSYGEVHVGDMFVSVPKADAVPMKWI CHDMSDAHCLKFLKNCYDALPENGKYLVE 298
DB 301 ILPVAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGPBGFRVAVASCAVNTW 360
299 ILPVAPDTSLATKGVVHIDVIMLANPGKERTKEFEALAKAGPBGFRVAVASCAVNTW 357
QY 361 IIEFLK 367
DB 358 VIEFLK 364

RESULT 4
US-08-204-288-2
Sequence 2, Application US/08204288
Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSELAERE, Jan
APPLICANT: FRITIG, Bernard J. M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-2

Query Match 82.1%; Score 1572.5; DB 1; Length 3
Best Local Similarity 80.3%; Pred. No. 2.8e-166;
Matches 294; Conservative 36; Mismatches 33; Indels 2;

QY 1 MGSTETKMSPEAAAEAEAFVPMOLTSASVLPVMTKSAIELDVLEIM 60
1 MGSTETQMTPTQ--VSDEAHLPANQLASASVLPMLTKTALIEDLLEIM 58
DB 61 TSDIASKLPTRKPDPAVMDRLRLASYSVLTCSLRTLPDGIKIERLYGL 120
59 TSEIASHLPTRKPDPAVMDRLRLRLASYSILTCSLKDLPDGIKIERLYGL 118
QY 121 DDGVSIALSLMNOCKVLMESWYHLTEAVLLEGIPFNKAYGWTAFEGHT 180
119 EDGVSVPCLMNOCKVLMESWYHLKDAILDGIIPFNKAYGWTAFEGHT 178
DB 181 GMSNSTITMKKILETYKGFEGISVVDVGSGTGALNMIIAKYPMIKGI 240
179 GMSDSTITMKKILETYKGFEGISVVDVGSGTGAVVNTIVSKYPSIKGI 238
QY 241 APSYGEVHVGDMFVSVPKGDALFMKNI CHDMSDEHCLKFLKCYEALP 300
239 APSYGEVHVGDMFVSVPKADAVPMKWI CHDMSDAHCLKFLKNCYDALP 298
DB 301 ILPVAPDASLPTKAVVHIDVIMLANPGKERTKEFEALAKAGPBGFR 360
299 ILPVAPDTSLATKGVVHIDVIMLANPGKERTKEFEALAKAGPBGFR 357
QY 361 IIEFLK 366
DB 358 VIEFLK 363

RESULT 5
US-09-500-569-4
Sequence 4, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca B.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-methyltransferase

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/ FILE REFERENCE: BB1327 US NA
/ CURRENT APPLICATION NUMBER: US/09/500,569
/ CURRENT FILING DATE: 2000-02-09
/ EARLIER APPLICATION NUMBER: 60/119,587
/ EARLIER FILING DATE: 1999-February-10
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 4
/ LENGTH: 365
/ TYPE: PRT
/ ORGANISM: Glycine max
US-09-500-569-4

Query Match      81.8%; Score 1566.5; DB 2; Length 365;
Best Local Similarity 80.2%; Pred. No. 1.3e-165;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSSTETKNSPSEAAAEAEAFVAMQLTASAVLPVNLKSAIEDLVLEIMAKAGPGAHIS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSSTETQITPTTH--VSDEANLFAWQLASASVLPMLILKSALELDLEITIAKAGPGVHLS 58

QY 61 TSDIASKLPKXNPDAVMDRLMLRLASVLTGSLRTIPDGKIERLYGLAPYCKFLTKN 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 PTDISSQLPTQNPDAVMDRLMLRLACVNLISFSLRTLPGDKVEKLYGLAPYAKYLTKN 118

QY 121 DDGVSIALSLMNQDKVLMESWYHLTEAVLLEGGIPFNKAYGNTAFETGTPRENTVFN 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 EDGVSIALSLMNQDKVLMESWYHLTKDAVLEGGIPFNKAYGNTAFETGTPRENTVFN 178

QY 181 GMSNHTITMKKILETYGFGFGLGSVDVGGTGAAHLMNIIAKYPMIKGINFDPHIVE 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 GMADHSTITMKKILETYGFGFGLGSVDVGGTGAVINMIVSKHPITKGINFDPHIVID 238

QY 241 APSYGEVHVGGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEALPDKGYTLAEC 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 APSYGEVHVGGDMFVSVPKADALFMKWI CHDMSDEHCLKFLKCYEALPDKGYTLAEC 298

QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPQKERTKEFEALAKAGFEGFRVVAACAINTW 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 ILPVPADSSSLATKGVVHIDVIMLAHNPQKERTKEFEALAKAGSGFRVVC-CAFNIN 357

QY 361 IIEFLKKI 368
   |||:|||||
Db 358 IMEFLKKI 365

RESULT 6
US-09-971-823B-4
/ Sequence 4, Application US/0971823B
/ Patent No. 6610521
/ GENERAL INFORMATION:
/ APPLICANT: Cahoon, Rebecca E.
/ TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
/ FILE REFERENCE: BB1327 US NA
/ CURRENT APPLICATION NUMBER: US/09/971,823B
/ CURRENT FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/119,587
/ PRIOR FILING DATE: 1999-02-10
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 4
/ LENGTH: 365
/ TYPE: PRT
/ ORGANISM: Glycine max
US-09-971-823B-4

Query Match      81.8%; Score 1566.5; DB 2; Length 365;
Best Local Similarity 80.2%; Pred. No. 1.3e-165;
Matches 295; Conservative 41; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGSSTETKNSPSEAAAEAEAFVAMQLTASAVLPVNLKSAIEDLVLEIMAKAGPGAHIS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSSTETQITPTTH--VSDEANLFAWQLASASVLPMLILKSALELDLEITIAKAGPGVHLS 58

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QY 61 TSDIASKLPKXNPDAVMDRLMLRLASVLTGSLRTIPDGKIERLYGL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 PTDISSQLPTQNPDAVMDRLMLRLACVNLISFSLRTLPGDKVEKLYGL 118

QY 121 DDGVSIALSLMNQDKVLMESWYHLTEAVLLEGGIPFNKAYGNTAFETG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 EDGVSIALSLMNQDKVLMESWYHLTKDAVLEGGIPFNKAYGNTAFETG 178

QY 181 GMSNHTITMKKILETYGFGFGLGSVDVGGTGAAHLMNIIAKYPMIG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 GMADHSTITMKKILETYGFGFGLGSVDVGGTGAVINMIVSKHPITK 238

QY 241 APSYGEVHVGGDMFVSVPKGDALFMKWI CHDMSDEHCLKFLKCYEAL 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 APSYGEVHVGGDMFVSVPKADALFMKWI CHDMSDEHCLKFLKCYEAL 298

QY 301 ILPVPADASLPTKAVVHIDVIMLAHNPQKERTKEFEALAKAGFEGFR 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 ILPVPADSSSLATKGVVHIDVIMLAHNPQKERTKEFEALAKAGSGFR 357

QY 361 IIEFLKKI 368
   |||:|||||
Db 358 IMEFLKKI 365

RESULT 7
US-08-204-288-5
/ Sequence 5, Application US/08204288
/ Patent No. 5959178
/ GENERAL INFORMATION:
/ APPLICANT: VAN DOORSELAERE, Jan
/ APPLICANT: FRITIG, Bernard J.M.
/ APPLICANT: INZE, Dirk G.
/ APPLICANT: JOUHANIN, Lise
/ APPLICANT: KNIGHT, Mary E.
/ APPLICANT: LEGRAND, Michel
/ TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
/ TITLE OF INVENTION: PLANTS
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D. C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3518
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/204,288
/ FILING DATE: 10-MAR-1994
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9119279.9
/ FILING DATE: 10-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/01460
/ FILING DATE: 09-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOKULIS, Paul N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 206860/SBB36543/UST
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202) 822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:

```

LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-5

Query Match 78.3%; Score 1499.5; DB 1; Length 364;
Best Local Similarity 77.8%; Pred. No. 3.9e-158;
Matches 281; Conservative 36; Mismatches 41; Indels 3; Gaps 2;

QY 1 MGSTSETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSSTESQ--SNSLTTEDEAFIPMQLCSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGLAPVCKELTEN 120
DB 59 PSLAAQLSTQNPDAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGLAPVCKELTEN 118
QY 121 DGVSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGTDPRENTVFN 180
DB 119 ADGVSAVAPLLNMQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGTDPRENTVFN 178
QY 181 GMSNSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGINFDLPVLEE 240
DB 179 GMSDSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGINFDLPVIGD 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 300
DB 239 APYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALPTNGKYLAE 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLANPGGKERTKFEALAKAGAFEGF-RVAVSCAYNT 359
DB 299 ILPEAPDSSLATKGVVHIDVIMLANPGGKERTKFEALAKAGAFEGF-RVAVSCAYNT 358
QY 360 W 360
DB 359 W 359

RESULT 8
US-09-500-569-18
Sequence 18, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafaleki, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-methyltransferase Homologs
FILE REFERENCE: B1327 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 358
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (134)
US-09-500-569-18

Query Match 77.9%; Score 1492; DB 2; Length 358;
Best Local Similarity 78.1%; Pred. No. 2.6e-157;
Matches 282; Conservative 39; Mismatches 36; Indels 4; Gaps 3;

QY 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 60
DB 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIMAKAGPGAHIS 58

QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGL 120
DB 59 PSLAAQLSTQNPDAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGL 118
QY 121 DGVSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGT 180
DB 119 EDGVSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGT 178
QY 181 GMSNSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGI 240
DB 179 GMSDSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGI 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALP 300
DB 239 APYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALP 298
QY 301 ILPVAPDASLPTKAVVHIDVIMLANPGGKERTKFEALAKAGAFEGF 359
DB 299 ILPEAPDSSLATKGVVHIDVIMLANPGGKERTKFEALAKAGAFEGF 358
QY 360 W 360
DB 358 W 358

RESULT 9
US-09-971-823B-18
Sequence 18, Application US/09971823B
Patent No. 6610521
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeic acid 3-O-methyltransferase
FILE REFERENCE: B1327 US NA
CURRENT APPLICATION NUMBER: US/09/971,823B
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/119,587
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 358
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (134)
OTHER INFORMATION: Xaa = ANY AMINO ACID
US-09-971-823B-18

Query Match 77.9%; Score 1492; DB 2; Length 358
Best Local Similarity 78.1%; Pred. No. 2.6e-157;
Matches 282; Conservative 39; Mismatches 36; Indels 4; Gaps 3;

QY 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIM 60
DB 1 MGSSTETKSPSEAAAEAFVAMQLTSASVLPVWLKSAIELDVLEIM 58
QY 61 TSDIASKLPTKQPDAAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGL 120
DB 59 PSLAAQLSTQNPDAVMDRLRLRLASVYLTSCLRTLPDGKIERLYGL 118
QY 121 DGVSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGT 180
DB 119 EDGVSIALLSLMNQDKVLMESWYHLTEAVLEGIPFNKAYGWTAFEGT 178
QY 181 GMSNSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGI 240
DB 179 GMSDSTITMKKILETYGFEGLSGVDVGGGTGAHLMMITAKYPMIKGI 238
QY 241 APSYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALP 300
DB 239 APYGVHVGDMFVSPKGDALFMKWI CHDMSDEHCLKFKCYEALP 298

QY 318 IDVIMLANHPGKERTKEFEALAKAGPREGFRVVASCAVNTWIIIEFLKX 367
DB 317 LDCHTLVHNGGSKERSKEDEFEALASKTGSTVDVIC-CAYDTWVWELTKK 365

RESULT 15
US-08-204-288-7
Sequence 7, Application US/08204288
Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSSELAERE, Jan
APPLICANT: FRITIG, Bernard J. M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-7

Query Match 54.6%; Score 1045.5; DB 1; Length 365;
Best Local Similarity 57.1%; Pred. No. 1,6e-107;
Matches 210; Conservative 51; Mismatches 96; Indels 11; Gaps 7;

QY 5 SETKMSPEAAAEAEAFVAFANQLTSASVLPMTLKSALIEIDVLEIMAKAGPQAHSITSDI 64
DB 3 SSTK-SQIPTQSEEBENCTYAMQQLSSSYLPFVTHSTIQLEVEFELIAKSN-DTKLSASQI 60
QY 65 ASKLPF-KNPDAVVMIDRMRLRLASYSVLTCSLRTLPD----GKIBRLGLAPVCKELTR 119
DB 61 VSOIPCKNPDATMIDRMRLYLASYSLFTCSI--VEDEENNGGQKRVYGLSQVGKFFVR 118
QY 120 NDDGVSIALLSMNQKVMESWYHLTEAVLEGIPFNKAYGWT-AFEYHGTDPRENTVF 178

DB 119 DEDGASWGPFLALALQDKVFINSWFELKDAVLEGGVFPDRVHGVVAFAFEXPI 178
QY 179 NNGMSNHSITIMKILLETYKGFEGLSVVDVGGGAGALNNIIAKYPMIK 238
DB 179 NKAMINHTTVMKILLENYKGFENIKTLVDVGGGLGVNLKMTSKYPTIK 238
QY 239 EADSPYGVENVGGDMFVSPKGDALFMKWI CHDWSDEHCLKFLKCYEAL 298
DB 239 QHAPSYGVENVGGDMFVSPVEGDALFMKWI LHDWSDSHNLKLNKCYKAI 298
QY 299 ECILPVADASLPTKAVVHIDVIMLANHPGKERTKEFEALAKAGFEGI 358
DB 299 EAILPVKPDIDTAVVGVSCDILIMMAQNPGGKERSSEEFALATEAGFKGI 358
QY 359 TWIIEFLK 366
DB 358 PWMEFCK 365

Search completed: December 12, 2005, 08:48:28
Job time : 48 secs